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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                    Score
            seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

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          GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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        1 US-09-867-570-2
US-09-995-225-20
0 US-09-995-225-20
1 US-10-183-116-31
2 US-10-125-567A-674
2 US-10-072-012-534
2 US-10-401-397A-2
3 US-10-072-012-530
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Sequence 2, Appli
Sequence 20, Appl
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Sequence 31, Appl
Sequence 514, App
Sequence 529, App
Sequence 534, App
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Length 337; Indels 0; Gaps 0; TLSFTGLTCIVSLYALTGN 60 TLSFTGLTCIVSLYALTGN 60 TLINITHPISKILSPVMTFP 120 LINITHPISKILSPVMTFP 120 WALSLLRSILEWMFCDFLF 180	ENCODING HUMAN GPCR	Sequence 10, Appl Sequence 528, App Sequence 532, Appl Sequence 10, Appli Sequence 4, Appli Sequence 20, Appl Sequence 12, Appl Sequence 172, Appl Sequence 172, Appl Sequence 527, Appl Sequence 527, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 18, Appl Sequence 174, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 22, Appl Sequence 24, Appl Sequence 24, Appl Sequence 27, App

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PRIOR PILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2000-12-12
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR PILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR PILING DATE: 2001-02-20
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Best Local Similarity
Matches 322; Conser
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Publication No.
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SOFTWARE: PatentIn version
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-07-31
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                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                  ENGTH: 322
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APPLICATION NUMBER: 60/282,356
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Chu, Zhi Liang
Dang, Huong T.
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  VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
                                               MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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                                                                                                                                       95.7%; Score 1688; DB 9; I ilarity 100.0%; Pred. No. 4.6e-145; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 322
TYPE: PRT
TYPE: PRT
TORGANISM: Artificial Sequence
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CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILLNG DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
Query Match
Best Local Similarity
Matches 322; Conserv
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APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR APPLICATION NUMBER: 60/290,917
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PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
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                                                                                                            FEATURE:
OTHER INFORMATION: No.
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vo. US20030139588A9
95.7%; Score 1688; DB 10; 100.0%; Pred. No. 4.6e-145; ive 0; Mismatches 0;
                                                                                                                         US20030139588A9el Sequence
                                               Length 322;
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APPLICANT: Anderson, David J.
APPLICANT: Eyika, Mark
APPLICANT: Zyika, Mark
APPLICANT: Zyika, Mark
APPLICANT: Zyika, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE 4C1CP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 69/704,707
PRIOR FILING DATE: 2001-04-19
PRIOR PILING DATE: 2001-04-9
PRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
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US-10-183-116-31
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Best Local Similarity
Matches 322; Conserv
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SEQ ID NO 31
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/ 100.0%; Pr
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APPLICANT: Burmer, Glenna C.

APPLICANT: ROUSH, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PK.

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT APPLICATION NUMBER: 60/257,144

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR FILING DATE: 2000-12-19

AUMBER 60/257,144

PRIOR FILING DATE: 2000-12-19

SOPTWARE: PATENTAL OF SEQ ID NOS: 2292

SOFTWARE: PATENTAL OF SEQ ID NOS: 2292

TYPE: PDT

COLUMN NUMBER: 60/257,144
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US-10-072-012-529
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US-10-225-567A-674
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Sequence 529, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
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Best Local Simi
Matches 322;
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100.0%; Fi
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US-10-072-012-529
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PRIOR FILLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR PELLING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR PELLING DATE: 2001-02-05
PRIOR PELLING DATE: 2001-02-05
PRIOR PELLING DATE: 2001-02-05
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SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 529
LENGTH: 322
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PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
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CURRENT FILING DATE: 2002-01-31
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APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
APPLICANT: Droteins and Nucleic Acids
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                       196 IAWLVFLCVVLCGSSLVLLVRILCGSRKWPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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                                                                                                                          136 CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
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                                                                                                                                                                                                                                                                                            1 MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
                                                                                              CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                                                                                                                                                                               VSIYILMLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                                                                                                                                                                                            VSIYILNLVAADFLFLSGHIICSFLRLINIRHFISKILSFVMTFFYFIGLSMLSAISTER 135
IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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Grosse, William M.
Alsobrook II, John P.
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Taupier Jr, Raymond J.
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Shimkets, Richard
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US-10-072-012-534
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SOFTWARE: Pate:
SEQ ID NO 534
FONGTH: 322
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CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
Query Match
Best Local Similarity
Matches 322; Conser
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                          LENGTH: 322
TYPE: PRT
ORGANISM: Homo #
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                                                                                                                                                                                                                    Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 1391
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/267,459 PRIOR FILING DATE: 2001-02-08
                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/265,395
PRIOR TILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgese, Catherine B.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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PRIOR FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 21402-258
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                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/267,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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Grosse, William M.
Alsobrook II, John P.
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Pena, Carol E. A
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95.7%; Score 1688; DB 15; larity 100.0%; Pred. No. 4.6e-145; Conservative 0; Mismatches 0;
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                                          Length 322;
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TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION AND TREATMENT OF ELEVATED
TITLE OF INVENTION: INTERACCULAR PRESSURE AND RELATED CONDITIONS
FELLE REFERENCE: 4518/1M674US1
CURRENT APPLICATION NUMBER: US(10/401,397A)
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/367,513
PRIOR PILLING DATE: 2002-03-27
NUMBER: 0F SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 322
TYPE: PRT
NRAANISM: Homo sapiens
US-10-401-397A-2
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US-10-401-397A-2
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Publication No. US20030212001A1
GENERAL INFORMATION:
APPLICANT: Moffett, Serge
APPLICANT: Moffett, Serge
APPLICANT: Abran, Daniel
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Best Local Similarity 99.7%;
Matches 321; Conservative
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                                                          RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                                                                                     CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
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Pred. No. 1.3e-144;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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| Publication No. US20030235833A1 |
| GENERAL INFORMATION: |
| APPLICANT: SUMA, MAKIKO |
| APPLICANT: SUMA, MAKIKO |
| APPLICANT: ASAI, KIYOSHI |
| APPLICANT: ABURATANI, HIROYUKI |
| TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS |
| FILE REFERENCE: 084335/166 |
| CURRENT APPLICATION NUMBER: US/10/292,798 |
| CURRENT FILLING DATE: 2002-11-13 |
| PRIOR APPLICATION NUMBER: 10/017,161 |
| PRIOR APPLICATION NUMBER: 10/017,161 |
| PRIOR APPLICATION NUMBER: JP 2001-12-18 |
| PRIOR APPLICATION NUMBER: JP 2001-12-18 |
| PRIOR APPLICATION NUMBER: JP 2001-246789 |
| PRIOR FILING DATE: 2001-06-18 |
| SOFTWARE: PRI CONTENT OF SEQ ID NOS: 2070 |
| SOFTWARE: PRI CONTENT OF SERVICE |
| SEQ ID NO 1274 |
| LENGTH: 322 |
| TYPE: PRI CONTENT OF SERVICE |
| TYPE: P
Sequence 530, Application US/100
Publication No. US/20040033493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Sethusen, Bryan
APPLICANT: Sethusen, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Badigaru, Muralidha
APPLICANT: Anderson, David W.
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US-10-072-012-530
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US-10-292-798-1274
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US-10-292-798-1274
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les 321; Conserv
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  Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
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b. US20040033493A1
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99.7%;
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Pred. No. 1.3e-144;
1; Mismatches 0;
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Rastelli, Luca Miller, Charles E.

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; ORGANISM: Homo sapiens
US-10-072-012-530
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SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 530
LENGTH: 322
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Best Local Similarity
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
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PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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FILING DATE: 2001-02-02
APPLICATION NUMBER: 60/266,767
FILING DATE: 2001-02-05
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VDEGGGWLPQETLELSGSRLEQ 337
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Grosse, William M.
Alsobrook II, John P.
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Rieger, Daniel K.
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Pred. No. 1.3e-144;
1; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-072-012-535
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US-10-072-012-535
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
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SEQ ID NO 535
LENGTH: 322
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Best Local Similarity
Matches 321; Conserv
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PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
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PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
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APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
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                                                                   16 MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
76 VSIYILNLVAADELELSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
                                           1 MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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Spytek, Kimberly
Zerhusen, Bryan
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Grosse, William M.
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Taupier Jr, Raymon
Gusev, Vladimir Y.
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Shimkets, Richard
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99.7%;
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Pred. No. 1.3e-144;
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APPLICANT: Nehls, Michael
APPLICANT: Wattler, Frank
ITITLE OF INVENTION: No. US0040038345A1el Human Sev
FILE REFERENCE: 7705.0008-00-000
CURRENT APPLICATION NUMBER: US/10/391,074
CURRENT FILING DATE: 2003-03-17
INUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 322
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Sequence 79, Application US/10219834 Publication No. US20030096751A1 GENERAL INFORMATION:
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Best Local Similarity 99.4%;
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                                                                                                                                                                                 241 RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                                                                                                                                                                                                                    196 IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 MDSTIPVLGTELTPINGREETPCYKQTLSPTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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                                                                                                                  VDEGGGQLPQETLELSGSRLEQ 322
                                                                                                                                                                                                      RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
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Pred. No. 8.5e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
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Sequence 10, Application US/10237467

publication No. US20030186324A1

general Information:

APPLICANT: Liao, Jiayu

APPLICANT: Gray, Nathanael S.

APPLICANT: Gray, Nathanael S.

APPLICANT: Caldwell, Jeremy C.

APPLICANT: Schultz, Peter G.

FILE REFERENCE: 021288-001300US

CURRENT APPLICATION NUMBER: US/10/237,467

CURRENT APPLICATION NUMBER: US/0/237,467

CURRENT APPLICATION NUMBER: US 60/317,879

PRIOR APPLICANTE PATENTIN VET. 2.1

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US-10-237-467-10
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local (
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TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THEF
FILE REFERENCE: D0191 NP
CURRENT APPLICATION NUMBER: US/10/219,834
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/333,417
PRIOR FILING DATE: 2001-11-26
PRIOR PPLICATION NUMBER: US 60/338,367
PRIOR PILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 192
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PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: US 60/340,703
PRIOR FILING DATE: 2001-10-30
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PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/355,596
PRIOR FILING DATE: 2002-02-06
PRIOR FILING DATE: 2002-02-06
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Local Similarity 97.5%;
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                                                                                        VDEGGGWLPQETLELSGSRLEQ 337
                                                                                                                                           RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQN----
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                                                                                                                                                              RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE 315
                                                                                                                                                                                                               IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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                                                                       VDEGGGWLPQETLELSGSRLEQ
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Pred. No. 1.3e-140;
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Best Local Similarity
Matches 301; Conser
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Publication No.
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TYPE: PRT
ORGANISM: Homo :
FEATURE:
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
                                         CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
                                                                                      APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids
FILE REFERENCE: 21402-258
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Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
Miller, Charles E.
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Zerhusen, Bryan
Patturajan, Meera
                                                                                                                                                                               Furtak, Katarzyna
Grosse, William M.
                                                                                                                                                                                                                                                      Gerlach, Valerie
Taupier Jr, Raymond
Gusev, Vladimir Y.
                                                                                                                                Lepley, Denise M.
Rieger, Daniel K.
                                                                                                                                                                                                         Colman, Steven D. Wolenc, Adam R. Pena, Carol E. A
                                                                                                                                                                                                                                                                                                                                                                                         Shimkets, Richard
                                                                                                                                                              Alsobrook II, John P
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93.5%;
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Pred. No. 3.
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.4e-133;
                                                                                                    Encoding
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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-072-012-528
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Best Local Similarity
Matches 279; Conserv
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SEQ ID NO 528
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PRIOR
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PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
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RR FILLING DATE: 2001-01-31

DR APPLICATION NUMBER: 60/265,412

DR FILLING DATE: 2001-01-31

DR APPLICATION NUMBER: 60/265,395

DR FILLING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-02-02
APPLICATION NUMBER: 60/266,767
FILING DATE: 2001-02-05
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Search completed: October 27, Job time: 133 secs 2004, 08:45:33

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A Geneseq_23Sep04:*
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1763
1 MESKSSWVIRLGFLSMDSTI......EGGGWLPQETLELSGSRLEQ 337
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	10	Description
1	1763	100.0	337	ۍ <u>ا</u>	AAU97598	Aau97598 Human G-p
N	1688		322	ω	AAY90761	Human
w	1688	95.7	322	ហ	ABJ04077	Human G
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7	1688	95.7	322	6	ABP81750	Human
8	1688	95.7	322	œ	ADH08535	MrgX3
9	1688	95.7	322	œ	ADO44602	Ado44602 Human HI7
10	1688	95.7	322	8	ADO29705	Ado29705 Human GPC
11	1688	95.7	560	7	ADF70481	Adf70481 Orphan re
12	1683	95.5	322	w	AAY90762	
13	1683	95.5	322	u	ADI16994	Adi16994 Human NOV
14	1683	95.5	322	v	ADI16999	Adi16999 Human NOV
15	1683	95.5	322	7	ADC86821	Human
16	1683	95.5	322	œ	ADF29105	Adf29105 Human GPC
17	1683	95.5	322	æ	ADO44604	Ado44604 Human HI7
18	1663	94.3	322	w	AAB14846	Aab14846 Human nov
19	1642	93.1	322	N	AAY30159	Aay30159 Human dor
20	1598	90.6	322	N	AAY30160	Human
21	1557	88.3	302	σ	ABP96695	Abp96695 Human G p
22	1415.5	80.3	1589	σ	ADI16996	Human
23	1415.5	80.3	1589	5	ADI16992	Adi16992 Human NOV
24	1405	79.7	322	N	AAY30161	Aay30161 Human dor
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new G-protein coupled receptor (GPCR) peptide. The invention is useful for identifying a modulator of GPCR of treating a disease or condition mediated by a human protease. The invention is also useful as models for the development of human therapeutics, for identifying therapeutic proteins, as targets for development of human therapeutic agents, and as query sequence to perform a search against sequence databases to, for e.g., identify other family members of related sequences. The vector of the invention is useful for producing a GPCR protein or peptide, for conducting cell-based assays involving the GPCR protein or its fragment, for identifying GPCR protein mutants whose functions are affected, and to produce non-human transgenic animals. The present amino acid sequence represents the human G-protein coupled receptor (GPCR) protein of the invention. This sequence is encoded by the human G-protein coupled receptor the human G-protein coupled receptor the human G-protein coupled the human G-protein coupled receptor (GPCR) gene located on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated G-protein coupled receptor peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise
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31-MAY-2001;
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Best Local Similarity
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                                                                                                                                                                                                                                 CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                                                                                                                                                                                                                                                                                                                                     VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                                                                                IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Terao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsui H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1688; DB 3;
Pred. No. 1.2e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein and encoding nucleic acid, useful treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:1.
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                                                                                                                                Query Match
Best Local S
Matches 322
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12-DEC-2000;
20-FEB-2001;
20-FEB-2001;
06-APR-2001;
06-APR-2001;
06-APR-2001;
                                                                                                                                                                                                      The present invention provides the protein and coding sequences of several human G-protein coupled receptors (GPCRs). These can be used in the identification of candidate compounds as receptor agonists or inverse agonists having applicability as therapeutic agents. The present sequencis a GPCR protein of the invention
                                                                                                                                                                                                                                                                                                 Novel endogenous and non-endogenous versions of G protein-coupled receptor useful for identification of candidate compounds as receptors or antagonists for use as therapeutic agents.
                                                                                                                                                                               Sequence 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31; hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                           Claim 37; Page 75-76; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2002.
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DB; ABT04875.
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322; Conserv
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CLSILWPIWYHCRRPRYLSSVMCYLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                      VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                   VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                                                  MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
                                                                                                MDSTIPVLGTELTPINGREETPCYKQTLSPTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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2000US-025366P.

2001US-0270266P.

2001US-0270286P.

2001US-0282356P.

2001US-0282358P.

2001US-0282358P.

2001US-0282358P.

2001US-0282358P.

2001US-0282358P.

2001US-0282358P.

2001US-0282358P.

2001US-0309208P.
                                                                                                                               95.7%; Score 1688; DB 5; ilarity 100.0%; Pred. No. 1.2e-172; Conservative 0; Mismatches 0;
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                                                                                                      Query Match
Best Local S
Matches 322
                                                                                                                                                                                                                                                     The invention relates to Mrg (mas-related gene) protein, which is a G-protein coupled receptor and drg-12 protein, which is a receptor. The invention is useful for identifying compounds that bind to it, especially agonists or antagonists. Administration of an agent (e.g. the identified agonist) that increases the expression of Mrg in a mammal may be used for treating impaired sensory perception in a mammal, especially pain. The antagonist may also be useful for treating impaired sensory perception in a mammal. The present sequence is human MrgX3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide, Mrg, which is a G-protein coupled receptor a isolated polypeptide, drg-12, which is also a receptor, useful for identifying agonists or antagonists for treating pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-2000; 2000US-022027P.
01-AUG-2000; 2000US-0222344P.
03-NOV-2000; 2000US-00704707.
19-APR-2001; 2001US-0285493P.
                                                                                                                                                                                                          Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Page 130; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2001; 2001WO-US014519
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mas-related gene; G-protein coupled receptor;
or; sensory perception; pain; analgesic; MrgX3
                                                                                                                                 Similarity
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                                                                                                   95.7%;
ilarity 100.0%;
Conservative
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                                                                                                   Score 1688; DB 5; 1
Pred. No. 1.2e-172;
0; Mismatches 0;
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02-FEB-2001

05-FEB-2001

07-FEB-2001

07-FEB-2001

08-FEB-2001

09-FEB-2001

15-FEB-2001

26-FEB-2001

27-FEB-2001

27-FEB-2001

27-FEB-2001

12-MAR-2001

14-MAR-2001

14-MAR-2001

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15-MAR-2001

15-MAR-2001

16-MAR-2001

16-MAR-2001

16-MAR-2001

16-MAR-2001

26-MAR-2001

26-MAR-2001
                                                                                                                                                                                                                                                                31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                        human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.
                                                                                                                                                                                                                                                                                                                      31-JAN-2002;
                                                                                                                                                                                                                                                                                                                                            06-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NOVX protein homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI16993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI16993 standard;
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                                        2001US-0267823P
2001US-0268974P
2001US-0271664P
2001US-0271839P
2001US-0272788P
2001US-0272788P
2001US-0275925P
2001US-0275947P
2001US-0275947P
2001US-0275959
2001US-0275959
2001US-0275959
2001US-0275959
2001US-0276448P
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2001US-0266767P.
2001US-0266975P.
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19-JUN-2001;
13-AUG-2001;
16-AUG-2001;
16-AUG-2001;
21-AUG-2001;
21-AUG-2001;
21-AUG-2001;
07-SEP-2001;
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29-MAY-2001
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2001US-0294473P.
2001US-029959P.
2001US-029959P.
2001US-0312809P.
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2001US-0312809P.
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2001US-0315470P.
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2001US-0318115P.
2001US-0318115P.
2001US-0318115P.
2001US-031874P.
2001US-0333379P.
2001US-033330308P.
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Tchernev VT. Spytek KA, Zerhusen BD, Patrurajan M, Li L, Gangolli EA, Padigaru M, Anderson DW, Raste Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wole Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rie ajan M, Shimkets RA; Rastelli L, Miller CE; Wolenc AR, Pena CEA; 1, Rieger DK, Burgess CE Burgess CE;

WPI; 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing õ

Disclosure; SEQ ID NO 529; 1498pp; English

This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical corphysiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for diverse pathological conditions. The purthermore in the treatment of diverse pathological conditions. The purthermore in the treatment of conditions as well as methods to modulate their conditions as well as methods to modulate their conditions are useful in the diverse pathological conditions. The purthermore in the treatment of conditions are useful in the love polypeptides, polynucleotides and antibodies are useful in the treating or preventing Novy-associated disorders, e.g. cardiomyopathy, contracted their conditions, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, cartiritis, Alzheimer's disease, infections, stroke, muscular dystrophy can epilepsy. Accordingly, these molecules have many activities including cytostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, neuroprotective, nootropic, antiartrhritic, hepatotropic, antiartrhritic, hepatotropic, antiartrhritic, hepatotropic, antiartrhritic, hepatotropic, antiarteriosclerotic, ancreding consultation, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein coffice of the invention. pharmacogenomics. of the invention.

Sequence 322

95.7%; Score 1688; DB Ģ Length 322;

Best Local Similarity

100.0%;

Pred. No. 1.2e-172;

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RESULT 6
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ID 116998
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31-JAN-2001
31-JAN-2001
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31-JAN-2001
02-FEB-2001
07-FEB-2001
07-FEB-2001
09-FEB-2001
15-FEB-2001
26-FEB-2001
27-FEB-2001
27-FEB-2001
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27-FEB-2001
11-MAR-2001
11-MAR-2001
11-MAR-2001
11-MAR-2001
11-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2002;
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2001US-0265395P.
2001US-0265511PP.
2001US-0265517P.
2001US-02667406P.
2001US-0266767P.
2001US-0267957P.
2001US-0267959P.
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2001US-0267959P.
2001US-027989P.
2001US-0271839P.
2001US-0271839P.
2001US-0275947P.
2001US-0275947P.
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2001US-0294473P.
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2001US-0332701P
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Li L, G Gerlach Furtak K Tchernev VT, ev VT, Spytek KA, Zerhusen BD, Patturaj Gangolii EA, Padigaru M, Anderson DW, h VL, Taupier RJ, Gusev VY, Colman SD, K, Grosse wM, Alsobrook JP, Lepley DM, Patturajan M, Shimkets RA; son DW, Rastelli L, Miller lman SD, Wolenc AR, Pena C epley DM, Rieger DK, Burge Pena CEA; , Burgess (Miller CE; B

WPI; 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing c treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue pharmacogenomics. or typing ဝူ

Disclosure; SEQ ID NO 534; 1498pp; English

This invention relates to a novel nucleic acids, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical CC or physiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel thuman and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polynucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclarosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome CC antistitis, Alzheimer's disease, infections, stroke, muscular dystrophy CC and epilepsy. Accordingly, these molecules have many activities including CC treatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, hammostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, cantiasthmatic, nephrotropic, antibacterial, virucide, antiparasitic, CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic, relaxant and anticonvulsant. In addition, they are useful in screening casays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also

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ABP81777 7
ABP8 2XX ABP8
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XX G DX
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        WPI; 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atterosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension; hypotension; renal ulcer.
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                                                                                          Burmer GC,
                                                                                                                                                                                                                                                           19-DEC-2001; 2001WO-US050107.
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                                                                                                                                                                                                                                                                                                                                                                           WO200261087-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human G protein-coupled receptor MrgX3 protein SEQ ID NO:674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP81750
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                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                   2003-046718/04
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                                                                                                                                               LIFESPAN BIOSCIENCES INC.
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                                                                                          Rough
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor; GPCR; antigenic peptide; gene therapy;
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                            diseases.
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Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an CC antibody against a particular GPCR, and in the production of specific CC antibody against a particular GPCR, and in the production of specific CC antibodies. The peptides and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CC GPCRs and antibodies are useful for diagnosing and designing drugs for CC treating immune-related diseases, immunological-related cell proliferative CC diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, CC atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoparthitis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculcosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunoassays and immunoassays and emmonoaconsis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification the present invention

Query Match Best Local S Matches 322; 16 щ Similarity VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA Conservative 95.7%; 0, Score 1688; DB 6; Pred. No. 1.2e-172; Mismatches .. Length 322; Indels 0 Gaps 135 60

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VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER

120

Sequence 322 AA;

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VDEGGGWLPQETLELSGSRLEQ

322

ADH08535 standard; protein; 322

ADH08535;

RESULT 8
ADH08535
ID ADH0
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AC ADH0
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DT 25-M
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Best Local S
Matches 322
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to an isolated mas-related gene D (MrgD) polypeptide. The MrgD polypeptides are useful as therapeutics or for identifying compounds, i.e. agonists or antagonists, that alter pain perception in a mammal. The compounds are useful for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain, promoting wound healing, restoring normal sensitivity following injury, or treating ocular conditions, particularly those associated with pressure such as glaucoma. The Mrg genes or proteins may be used as molecular probes for the detection of cells or tissues related to or involved with sensory perception. The present sequence represents a MrgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New mas-related gene D polypeptides, useful as therapeutics or in identifying agonists or antagonists that alter pain perception in a mammal for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain.
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 322
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sensory perception;
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DB; ADH08534.
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                                                                                                                                                                                                                                            76 VSIYILNLVAADFLFLSGHIICSFLRLINIRHPISKILSFVMTFPYFIGLSMLSAISTER
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                   VDEGGGWLPQETLELSGSRLEQ 337
                                                       RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                          RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                                                           CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
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VDEGGGWLPQETLELSGSRLEQ 322
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100.0%; Pr
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glaucoma; Mrg.
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RESULT

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Best Local Similarity
                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                  The invention relates to a non-human mammal that carries a DNA integrated with a foreign HI77213 or its mutant gene, or a part of it. The non-human animal is particularly a rat. Such gene shows phenotypes of e.g. cataract conset, transient skin rash and proliferation-promoting activity. The foreign HI77213 gene is a gene that encodes a G protein-coupled receptor (GPCR) protein HI77213. The protein, its encoded DNA and constructed transgenic animals are useful for clarifying pathological mechanism, developing therapeutic methods and screening preventives or remedies for related diseases e.g. cataract, cancer, and dermatitis. The present sequence represents a human HI77213 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HI7T213 protein, encoded DNA and transgenic animals for clarifying pathological mechanism, developing therapeutic methods and screening preventives or remedies for related diseases e.g. cataract, cancer, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HI7T213; transgenic; G protein-coupled receptor; GPCR; ophthalmological; cytostatic; nephrotropic; antiinflammatory; dermatological; analgesic; vulnerary; neuroprotective; human; receptor.
                                                                                                                                                                                                                                                                                               Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; SEQ
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                                                                                                                                       RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                 CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILBWMFCDFLFSGADSVWCETSDFIT
                                                                                      CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMPCDFLFSGADSVWCETSDFIT
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                                                                                                                                                                                                                                                       Score 1688; DB 8;
Pred. No. 1.2e-172;
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  mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; bone disorder; joint disorder; metabolic disorder; mutritive disorder; bone disorder; kidney disorder; liver disorder; lung disorder; breast disorder; kidney disorder; ruterus disorder; lung disorder; testis disorder; ovary disorder; ruterus disorder; prostate disorder; stemach disorder; prostate disorder; pelen disorder; skin disorder; thyroid disorder; antiparkinsonian; antimanic; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; cortostatic; antiinflammatory; vasotropic; antianginal; antiseborrhoeic; virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antibleer; antibacterial; antianaemic; antiseborrhoeic; dermatological; antibleer; antibacterial; antianaemic; antopic; humanical; antiseborrhoeic;
                                                                                                                                                                                               The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                      Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder;
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09-APR-2003; 2003US-0461329P.
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                                                                                                                                                                                                                                                                                                                                                             SEQ
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  depression, diabetic neuropathy, disorders of the adrenal gland; c
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VDEGGGWLPQETLELSGSRLEQ 322
                                                                            RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                                                  RIHLDWKYLFCHVHLVSIFLSALNSSANFIIYFFVGSFRQRQNRQNLKLVLQRALQDTFE
                                                                                                                                                      IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
                                                                                                                                                                          IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
                                                                                                                                                                                                                                                                                                                                                                                    MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
                                  VDEGGGWLPQETLELSGSRLEQ
                                                                                                                                                                                                                                  CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95.7%; Score 1688; DB 8; 100.0%; Pred. No. 1.2e-172;
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ADF70481 standard; protein; 560 AA.

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ADF70481;

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ADF70481;

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DT 12-FEB-2004 (first entry)

XX

VX

DT 12-FEB-2004 (first entry)

XX

VX

DE Orphan receptor ligand-related human protein SeqID104.

XX

XX

XX

Ligand; orphan receptor protein; fusion protein; fluorescent protein; KW

Cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;

XX

XX

XX

MC GFPuv; Enhanced GFP; EGFP; human.

XX

VX

VX

VX

VB Homo sapiens.

XX

VX

VB -AUG-2003.

XX

Z1-FEB-2003; 2003WO-JP001901.

XX

Z2-FEB-2002; 2002JP-00045728.

PR 23-JUL-2002; 2002JP-00249237.
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RESULT 12
AAY90762
ID AAY90
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AC AAY90
DT 18-AU
DT 18-AU
XX
WW Human
XX
Human
XX
Genet
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Homo
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Homo
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Best Local (
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                                                                                                                                                                     Human; G protein-coupled receptor; hippocampus; diagnosis; screening; genetic disease; cellular function regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel method of identifying ligands to orphan receptor protein which comprises transforming cells with DNA
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                                                                                                                                                                                                                                                   Human G protein-coupled receptor hHI7T213V SEQ ID NO:2
                                                                                                                                                                                                                                                                                                             18-AUG-2000
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                                                                                                                                                                                                                                                                                                           entry)
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Pred. No. 2.4e-172;
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13-APR-2000

ADI16994
ID ADI16
XX
AC ADI16

standard;

protein;

322

15-APR-2004 ADI16994 ADI16994

(first

entry)

human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;

Human NOVX protein homologue SeqID 530

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human-derived G protein-coupled protein and encoding nucleic acid, useful e.g. in determining ligands and treatment of diseases associated with dysfunction of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human-derived G protein-coupled protein designated hH17T213V, which is isolated from the human hippocampus. The G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 92-93; 97pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                             321; Conservative
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                VDEGGGWLPQETLELSGSRLEQ 337
                                                                              RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTEE 315
                                                                                                                                                                                                       CLSILWPIWYHCRRPRYLSSVMCVLLWALSILRSILEWMFCDFLFSGADSVWCETSDFIT
                                                                                                                                                                                                                                                                     VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                               RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                                                                                            IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
                                                                                                                                                                                        CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGANSVWCETSDFIT
                                                                                                                                                                                                                                                    VSIYILNLVAADFLELSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
VDEGGGWLPQETLELSGSRLEQ
                                                                                                                            IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-JP005366
                                                                                                                                                                                                                                                                                                                                                                                            95.5%;
                                                                                                                                                                                                                                                                                                                                                                             1:
                                                                                                                                                                                                                                                                                                                                                                             Score 1683; DB 3;
Pred. No. 4.1e-172;
1; Mismatches 0;
322
                                                                                                                                                                                                                                                                                                                                                                                                           Length 322;
                                                                                                                                                                                                                                                                                                                                                                                Indels
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31-JAN-2001
31-JAN-2001
31-JAN-2001
31-JAN-2001
02-FEB-2001
07-FEB-2001
09-FEB-2001
09-FEB-2001
11-FEB-2001
26-FEB-2001
27-FEB-2001
27-FEB-2001
11-MAR-2001
11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2002;
                                                       CURAGEN
                                                                           2001US-0265395P

2001US-0265412P

2001US-0265517P

2001US-0266767P

2001US-0266767P

2001US-0267679P

2001US-0267859P

2001US-0271668974P

2001US-0271858P

2001US-0271858P

2001US-0271858P

2001US-0277948P

2001US-0275945P

2001US-0275945P

2001US-0276450P

2001US-0276450P

2001US-0276450P

2001US-0276759P

2001US-0277875P

2001US-0277879P

2001US-0278775P

2001US-028959P

2001US-0285749P

2001US-029954P

2001US-029954P

2001US-0312889P

2001US-0312889P

2001US-03128470P

2001US-03118115P

2001US-03181115P

2001US-0318740P

2001US-0313390P

2001US-0313379P

2001US-0333308P

2001US-0333308P

2001US-0333308P
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                                                        CORP
Rastelli L, Miller Wolenc AR
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Sequence

322

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This invention relates to a novel nucleic acids, and encoded polypeptides core thereof, which have properties related to the stimulation of biochemical core physiological responses in a cell, tissue, organ or organism.

CC Specifically, it refers to the use of biologically active fragments for conditions. The present invention describes novel the use and furthermore in the treatment of conditions. The present invention describes novel than and murine NOVX protesias, as well as methods to modulate their compression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polynucleotides and antibodies are useful in comparison or preventing NOVX-associated disorders, e.g. cardiomyopathy, cratering or preventing NOVX-associated disorders, e.g. cardiomyopathy, ctreating or preventing diseases such as inflammation, autoimmune comparison of the preventing diseases such as inflammation, autoimmune comparison, obesity, asthmatic, immunoglobulin (Ig)A nephropathy, cirrhosis, cardiant, antiinflammatory, immunosuppressive, antialization, cytostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, cantisative, nortopic, antibaterial, virucide, antiparasitic, cardiant, antinflammatory, immunosuppressive, antialization, cellulated assays to identify small molecules that modulate or inhibit, for example, cardiant and anticonvolsant. In addition, they are useful in screening considers as in chromosome mapping, tissue typing, preventive medicine and plantancegenomics. This polypeptide is a homologue of a human NOVX protein
                                       pharmacogenomics.
of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful treating NOVX-associated disorders, e.g. cancer atherosclerosis, or diabetes, and in chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmacogenomics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
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5 片 S 밁 S 밁 ঠ 문 δ 밁 5 Best Loca Matches Query Match Local 136 301 316 241 181 196 121 321; 2 76 16 ш Similarity MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA CLSILWPIWYHCRRPRYLSSVMCVILWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS VDEGGGWLPQETLELSGSRLEQ VDEGGGWLPQETLELSGSRLEQ IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGANSVWCETSDFIT Conservative 95.5**%;** 99.7**%;** Score 1683; DB 5; Pred. No. 4.1e-172; L; Mismatches 0; 322 337 <u>,</u> Length Indels ٥, 300 240 180 120 135 60

Tchernev VI,

ev VT, Spytek KA; Zerhusen BD, Gangolli EA, Padigaru M, Ander h VL, Taupier RJ, Gusev VY, Cc

n BD, Patturajan M, Anderson DW, Raste Y, Colman SD, Wole

Miller CE; Pena CEA;

RESULT 14 ADI16999 ID ADI16 XX

ADI16999

standard; protein; 322

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19- FEB-2001
26- FEB-2001
27- FEB-2001
27- FEB-2001
27- FEB-2001
02- MAR-2001
14- MAR-2001
14- MAR-2001
14- MAR-2001
15- MAR-2001
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15- MAR-2001
16- MAR-2001
26- MAR-2001
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29- MAR-2001
21- APR-2001
21- AUG-2001
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31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
02-FEB-2001;
05-FEB-2001;
07-FEB-2001;
07-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabe inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
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                                                                                                                                                                               2001US-0280147P.
2001US-0282992P.
2001US-0283083P.
2001US-0285133P.
2001US-028832749P.
2001US-0288327P.
2001US-0288327P.
2001US-028832P.
2001US-02947P.
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2001US-02947P.
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2001US-0276450P.

2001US-027639P.

2001US-0276768P.

2001US-0278652P.

2001US-0278775P.

2001US-0278778P.

2001US-0278778P.

2001US-0278778P.

2001US-0279884P.

2001US-0279884P.
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2001US-0273046P
2001US-027592P
2001US-0275947P
2001US-027594P
2001US-0275950P
2001US-0275989P
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2001US-0271839P.
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2001US-0268974P.
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2001US-0267459P.
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2001US-0266767P.
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2001US-0312020P.
2001US-0312889P.
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2001US-0265517P.
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Gerlach
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                                                                                                                                                                                                               ev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
h VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CI
                                                                                                                                                                                                                 Burgess CE;
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New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing atherosclerosis, pharmacogenomics. õ

Disclosure; SEQ ID NO 535; 1498pp; English

CC or physiological responses in a cell, tissue, organ or organism.
CC specifically, it refers to the use of biologically active fragments for CC diverse pathological conditions. The present invention describes novel CC diverse pathological conditions. The present invention describes novel CC human and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polymucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome CC (AIDS), obesity, asthma, immunoglobulin (1g)A mephropathy, cirrhosis, CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy CC ard epilepsy. Accordingly, these molecules have many activities including Cryostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, cardiabetic, antiarteriosclerotic, anorectic, CC antiasthmatic, nephrotropic, antibacterial, virucide, antiparasitic, curvalent and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, CC used as in chromosome mapping, tissue typing, preventive medicine and CC of the invention. This polypeptide is a homologue of a human NOVX protein of the invention. This invention relates to a novel nucleic acids, and encoded thereof, which have properties related to the stimulation of polypeptides biochemical

Sequence ₽,

Similarity

95.5%;

Length 322; Indels

Gaps

밁 S 밁 Ś 밁 Ś 5 밁 밁 S Query Match Best Local S Matches 321 316 VDEGGGWLPQETLELSGSRLEQ 181 196 121 136 321; 61 76 RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPB IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPEGIQWALFS CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER RIHLDWKVLFCHVHLVSIFLSALNSSANFIIYFFVGSFRQRQNRQNLKLVLQRALQDTPB CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGANSVWCBTSDFIT IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS Conservative Score 1683; DB 5; Pred. No. 4.1e-172; 1; Mismatches 0; 0; 315 240 180 195 120 60 75

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VDEGGGWLPQETLELSGSRLEQ 322

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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 321; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The protein sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; SEQ ID NO 1274; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suwa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JAN-2003.
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               256 RIHLDWKVLFCHVHLVSIFLSALNSSANFIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE 315
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                                                                               196 IAWLVFLCVVLCGSSLVLLVRILCGSRXWPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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                                                                                                                                                                                                VSIYILMLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                                                                                                                                                                                 VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
                                                                                                                                                                                                                                                               MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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99.7%;
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Search completed: October 27, 2004, 08:30:17 Job time : 160 secs

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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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; SEQ ID NO 3
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-3
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APPLICANT: Banville, Denis
APPLICANT: Benville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat
FILE REFERENCE: 81823/268117
CURRENT FILLING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
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Best Local Similarity
Matches 313; Conserv
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          301
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ALIGNMENTS

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256 RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPB
                                                                                 76 VSIYILNLVAADFLFLSGHIICSFLRLINIRHPISKILSFVMTFFYFIGLSMLSAISTER
                                                                                                                                                                         61 VSIYILNLVAANFLFLSGHIIFSPLPLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
          VDEGGGWLPQETLELSGSRLEQ 337
VDEGGGWLPQETLELSGSKLEQ
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                       93.1%; Score 1642; DB 4; 97.2%; Pred. No. 8.7e-138;
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Length 322;

Rat

and

Human

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Sequence 7, Application US/09254227A

Patent No. 6696257

GENERAL INFORMATION:

APPLICANT: Abmad, Sultan

APPLICANT: Banville, Denis

APPLICANT: Lembo, Pacla

APPLICANT: Lembo, Pacla

APPLICANT: Lembo, Pacla

APPLICANT: Shi-Hsiang, Shen

TITLE OF INVENTION: G Protein-Coupled Receptors fro

FILS REFERENCE: 81823/268117

CURRENT APPLICATION NUMBER: US/09/254,227A

CURRENT FILING DATE: 199-03-03

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.0

SEQ ID NO 7

LENGTH: 322
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Patent No. 6696257

GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Hanville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: Lembo, Paola
APPLICANT: Shi-Halang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors fro
FILE REFERENCE: 81823/268117

CURRENT APPLICATION NUMBER: US/09/254,227A

NUMBER OF SEQ ID NOS: 22

SOFTMADE: APPLICATION STEP 199-03-03

NUMBER OF SEQ ID NOS: 22
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US-09-254-227A-7
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Best Local Similarity 95.6%;
Matches 307; Conservative
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GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Heiang, Shen
ITILE OF INVENTION: G Protein-Coupled Receptors from the Reference: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 199-03-03
NUMBER OF SEQ ID NOS: 22
COPPMANE: PERSTANTING PROSECUE AND AND ADDRESSED IN NOS: 22
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US-09-254-227A-7
                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 9
LENGTH: 322
TYPE: PRT
ORGANISM: Homo mapiens
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 270; Conserv
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Patent No. 6696257
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ORGANISM: Homo sapiens
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                                                                                                                               61 FSIYILNLAAADFLFLSGRLIYSLLSFISIPHTISKILYPVMMFSYFAGLSFLSAVSTER 120
                                                                                                                                                         76 VSIYILMLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
                                                                                                                                                                                                                                                16 MDSTIFVLGTELTFINGREETFCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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                                                                                                                                                                                                                                                                                                                          78.9%; Score 1391; DB 4; 83.9%; Pred. No. 1.5e-115;
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RESULT 6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-11
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 Sequence 13, Application US/09254227A
Patent No. 6656257
GENERRAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ahmad,
APPLICANT: Banvill
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Best Local Similarity
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SEQ ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
FILE REPLICATION NUMBER: US/09/254,227A
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                  CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILBWMFCDFLFSGADSVWCETSDFIT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSIYILNLVAADPLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
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Ahmad, Sultan
Banville, Denis
Fortin, Yves
Lembo, Paola
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Lembo, Paola
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Banville, Den
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83.4%;
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; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G Protein-Coupled Receptors from the
; FILE REFERNCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/09/254,227A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTMARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-227A-13
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                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin ve
SEQ ID NO 1
LENGTH: 337
TYPE: PRT
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                                                                                                                         ; ORGANISM: rat
US-09-254-227A-1
                                                           Query Match
Best Local S
Matches 174
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Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
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Best Local Similarity
                                                                                                                                                                                                                             APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
                                                           Local Similarity
nes 174; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDEGGGWLPQETLELSGSRL 335
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                                                                                                                                                                                                    PatentIn version 3.0
                                                             Conservative
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                                                           47.3%; Score 834.5; DB 4
52.9%; Pred. No. 3.3e-66;
tive 52; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                                                                                          DB 4;
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                                                                                           Length
                                                              Indels
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                                                              Gaps
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RESULT 8
5320941-2
;Patent No.
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US-08-118-270-52
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POLYPETIDES ENCODED THEREFROM AND DIAGNOSTIC AND OTHER METHODS
PARTICLES OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/872,087
FILING DATE: 06-JUN-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID
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                                                                                                              Sequence 52, Appli
Patent No. 5508384
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Best Local Similarity
                                                                                                GENERAL INFORMATION:
             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 RKAISVYVLNLSLADSFFLCCHFIDSLMRIMNFYGIYAHKLSKEILGNVAFIPYISGLSI 130
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                                                                                                                                                                                                                 SSANNFIYFFVGSSKKKRFKQSLKVVTTRAFKD
                                                                                                                                                                                                                                             SSANPIIYFFVGSFRQRQNRQNLKLVLQRALQD 312
                                                                                                                                                                                                                                                                                 NTWASHSSKLYIVIMVTIIIFLI----FAMRMRLLYLLYYEYWSTFGNLHDISLLFSTIN
                                                                                                                                                                                                                                                                                                                                                 LVTTMEYVMCIHTEEBSDS----PNDCPAVIIFIAILSFLVFTGLMLV-SSTILVVKIPK 216
                                                                                                                                                                                                                                                                                                                                                                                  LRSILEWMFCDFLFSGADSVWCBTSD-----FITI-AWLVFLCVVLCGSSLVLLVRILC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | SPVGFVENGILLWFLCFRMRRNPFTVYITHLSIADISLLFCIFILSIDYALDYELSSGH 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LORALODTPEVDEGGGWLPQETLELSGSR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYLFLLYWFGIHLHYP--FCHIYQVTVLLSCVNSSANPIIYFLVGSFRHRKKHRSLKMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIQWAL--FSRIHLDWKYLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSAISTERCLSVLWPIWYHCHRPRNMSAIICVLIWVLSPLMGILDWFFSGFLGETHHHLW
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                                                                                                                                                                                                                                                                                                                GSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALN
                                                                                                                                Application
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                                                            Murphy, Randall B. Schuster, David I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.0%;
               POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF 348
                                                                                                                                 US/08118270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 423.5; DB 6; pred. No. 8.4e-30; 58; Mismatches 93;
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Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/118
FILING DATE: 09-5EP-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REGISTRATION NUMBER: 4,033
STREET: 412 CITY: Washington
                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 4:
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419 Seventh Street, N.W.,
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34.4%;
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RESULT 10
PCT-US93-08528-52
Sequence 52, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND ME
                                                                                                                                                                                                                                                                                                224 LFSTINSSANPFIYFFVGSSKKKRFKESLKVVLTRAFKD
                                                                                                                                                                                                                                                                                                                           274 FLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQD 312
                                                                                                                                                                                                                                                                                                                                                                                                                                          214 LVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSI 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 SSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFITIAWLVFLCVVLCGSSLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 H-----YYTIVTLSVTFLFGYNTGLYLLTAISVERCLSVLYPIWYRCHRPKYQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 HIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRRPRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 VSLVALTGNAVVLW------------LIGCRMRRNAVSIYILNL-VAADFLFLSG
                                                                                                                                                                                                                                                                                                                                                                                               VVKIRKNTWASHSSKLYIVIMVTIIIFLIFAMPMRLLYYLLYYEY---WST-FGNLHHISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SALVCALLWALSCLVTTM-YVMCIDRFEESHSRNDCRAVIIFIAILSFLVFTPSVSSTIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 388.5; DE Pred. No. 9e-27;
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                                                                                         COMPOSITIONS AND METHODS THEREOF
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Suite 300
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MEDIUM TYPE:

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RESULT 11
US-08-118-270-76
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                                                                                                                                                                                                                          Sequence 76, Application US/08118270 Patent No. 5508384 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                STREET: 415
CITY: Washington
CTATE: D.C.
TYPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/
PILING DATE: 09-SEP-1993
                                                                                                                                                      APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OP INVENTION: POLYEPTIDES OF G-COUPLED PROTEIN
TITLE OP INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKST NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                     NUMBER OF SEQUENCES: 3
ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 20004
                              COUNTRY: USA
                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                    224 LFSTINSSANPFIYFFVGSSKKKRFKESLKVVLTRAFKD 262
                                                                                                                                                                                                                                                                                                                                                                      274 FLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQD 312
                                                                                                                                                                                                                                                                                                                                                                                                                       168 VVKIRKNTWASHSSKLYIVIMVTIIIFLIFAMPMRLLYLLYYEY---WST-FGNLHHISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 LVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSI 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 HIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRRPRYL 153
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                                                                                     419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 amino acids
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                                                                                                       BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMBER: US 07/943,236
10-SEP-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.0%; Score 388.5; DB 34.4%; Pred. No. 9e-27;
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                                                                                      Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
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PCT-US93-08528-76
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                                                                                                                                                                                                                                                                                         Sequence 76, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPETIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                   STREET: 419 C...
STREET: Washington
STATE: D.C.
STATE: USA
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: FORM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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LENGTH: 298 amino acid
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REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MUJ
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
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STRANDEDNESS: sir
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                                                                                                                           ZIP: 20004
                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 RDLCICINSSAKPIVYFIAGRDKSQRLWEPLRVVFQRALRDGAEPGDAASSTPNTVTMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 SIFLSALNSSANPITYFFVGSFRQRQNRQNLKLVLQRALQDTPEVDEGGGWLPQB-TLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 VRILCGSRKMPLT-RLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDW--KVLFCHVHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 LLWALSLLRSILEWMFCDFLFSGADSVWCETSDFITIAWLVF-----LCVVLCGSSLVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 RHPISKI-----LSPVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRRPRYLSSVMCV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 LTCIVSLVALTGNAVVLWILGCRMRNAVSIYI--LNLVAADFLFLSGHIICSPLRLINI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GTFLGSFPDYVRRVSRIVGLTFFAGVSLLPAISIERCVSVIFPMWYWRRRPKRLSAGVCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 19.5%; Score 344; DB 1; Length 29 1 Similarity 31.3%; Pred. No. 8.4e-23; 94; Conservative 58; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LLCLCGLV---GNGLVLWFFGFSIKRTPFSIYIYFLHIASADGIYLFSKAV---IALLNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHVECRARRRORSAKLNHVVLAIVSVFLVSSIYLGIDWFLF-----WVFQIPAPFPEYV
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                                                                                                                                                                                                          E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: single
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                                                                                                                                                                                                                                                                          348
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                     #1.0,
                     Version #1.25
                                                                                                                                                                                                                                                                                                COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                              Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sequence 6, Application US/08981825

Patent No. 6040426

GENERAL INFORMATION:
APPLICANT: OGAWA, KAZUYAUKI
APPLICANT: TANAKA, KAZUYA
APPLICANT: TAKANO, KYOICHI
APPLICANT: TAKANO, SYOICHI
TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
TITLE OF INVENTION: Th2, GENE (B19) ENCODING THE
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-981-825-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: [
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-
                                                                                                                                                    COUNTRY: U
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 VRILCGSRKMPLT-RLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDW--KVLFCHVHLV 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 RHPISKI-----LSPVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRRPRYLSSVMCV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 LLWALSLLRSILEWMFCDFLFSGADSVWCETSDFITIAWLVF-----LCVVLCGSSLVLL 214
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linear
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                                                                                                                                                                                                                                                                                                                         ENCODING THE SAME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 298;
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US-09-480-784-6
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                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Applicatio patent No. 6166186 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 395 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Altman, Daniel B
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: MS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: /13
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                                           COMPUTER READABLE FORM
                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                               TITLE OF INVENTION: PROTEIN SPECIFIC TO HUMAN
Th2, GENE (B19) ENCODING
                                                                                                                                                                                                                                                                                                                                             APPLICANT: OGAWA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317
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                                                                                                         CITY: Newport Beach STATE: CA
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                                                               COUNTRY: U.S.A.
ZIP: 92660
  MEDIUM TYPE: Diskette COMPUTER: IBM Compatible
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ilarity 25.9%;
Conservative 5
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NAGATA, KINYA
TAKANO, SYOICHI
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                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Murphy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                  APPLICANT: Murphy, Philip M.
TITLE OF INVENTION: Cloning of cDNA Encoding a Functional
TITLE OF INVENTION: Human Interleukin-8 Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman, Darby & Cushman
STREET: 1615 L Street, N.W.
COMPUTER READABLE FORM:
                                                                          STREET: 1615 L STREET: Washington
                   COUNTRY: USA
ZIP: 20036-5601
                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 395 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: MSHIM4.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/480,784
PILING DATE: 10-Jan-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 QNLKLVLQRALQDTPEVDEGG 320
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148 AHKVCLVLWALAVLNTVPYFVFRDTISRLDGRIMCYYNVLLLNPGPDRDATCNSRQAALA 207
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                                                               D.C
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FILING DATE: <Unknown>
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Search completed: October 27, 2004, 08:34:18
Job time : 41 secs

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TELEPAX: 202-822-0944
TELEX: 6714627 cush
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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NAME: Scott, Watson T.
REGISTRATION NUMBER: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US FILING DATE: 19910913 CLASSIFICATION: 435
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TOPOLOGY: line
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310
                                                                 256
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                                                                                                                                                            196 IAWLVFLCVVL-----CGSSLVLLVRILC-GSRKMPLTRLYV------TILLTVLVF
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                               288 FFVGSFRQRQNRQN--LKLVLQRAL 310
                                                                                                                                    200 AKW----CMVLRILPHTFGFILPLLVMLFCYGFTLRTLFQAHMGQKHRAMRVIFAVVLIF 255
                                                                                                                                                                                                                                   137 LSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWC-ETSDFIT 195
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                                                                                                                                                                                                                                                                                                                                       23 TGMPPVE-KDYSPCLVVTQTLNKYVVVVIYALVPLLSLLGNSLVMLVILYSRSNRSVTDV
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                                                                                                                                                                                                                                                                                                                                                                                                          94;
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                                                                                                  LLCGLPFG-----
                                                                                                                                                                                                                                                                    YLLNLAMAP-AFCPDHAYLGRLQGKRLDFRTPLCKVVSLVKEVNFYSGILLLACISVDRY 140
 AFIG---
                                                                 LLCWLPYNLVLLADTLMRTHVIQETCQRRNELDRALDATEI ----- LGFLHSCLNPIIY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 amino acids
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-ONFRNGFLKMLAARGL
                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 235.5; DB 1 28.9%; Pred. No. 4.2e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                          53; Mismatches 121;
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                                                                                                IQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIY 287
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78 81

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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                                                                                                                                                                          seq length: 0
seq length: 2000000000
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1763
                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                283416 seqs, 96216763 residues
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                                                                                                                                                                                                                                                                                                                                                          1 MESKSSWVIRLGFLSMDSTI......EGGGWLPQETLELSGSRLEQ 337
PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyright
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831.412 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	11.3	11.3	11.4	11.4	11.4	11.6	11.6	11.7	11.7	11.7	11.7	11.9	11.9	11.9	12.2	12.2	12.3	12.5	12.5	12.5	12.8	13.4	13.5	13.6	21.0	24.3	24.4	25.3	26.1	Match	Query
;	380	369	380	352	380	380	333	355	380	369	384	356	363	473	388	346	351	369	369	358	360	354	353	355	343	324	325	324	378	Match Length	
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	JC2338	B41795	JC2434	A46520	A55259	A48227	I65989	A55733	S36143	JC2083	A47249	S42096	157940	JC5835	JN0605	S29248	B42009	A45291	D41795	A53752	A53611	A23669	C42009	JQ1231	A35639	S51001	TVHUAS	TVRTAS	A39485	ID	
			kappa opioid recep	N-formyl peptide r	원	kappa opioid recep	G protein-coupled	_		somatostatin recep	brain-specific som	interleukin-8 rece	somatostatin recep	anaphylatoxin C3a	somatostatin recep	somatostatin recep	FMLP-related recep	somatostatin recep	somatostatin recep	interleukin-8 rece	interleukin-8 rece	interleukin-8 rece	FMLP-related recep	interleukin-8 rece					pro	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
186	186	187	187	187.5	188	189	193	193.5	194	194	194.5	196	196.5	196.5	196.5
10.6	10.6	10.6	10.6	10.6	10.7	10.7	10.9	11.0	11.0	11.0	11.0	11.1	11.1	11.1	11.1
391	391	378	340	352	359	392	364	375	364	363	350	384	504	371	350
2 C41795	2 A41795	2 A55735	2 JC7695	1 827357	2 149341	2 \$65693	2 A49542	2 JC5069	2 JN0763	2 157955	2 A39445	2 JC4629	2 A41783	2 JC5498	1 A37963
somatostatin recep	somatostatin recep	G protein-coupled	G protein-coupled	complement C5a ana	MIP-1 alpha recept	opioid receptor mu	N-formyl peptide c	G protein-coupled	somatostatin recep	somatostatin recep	interleukin-8 rece	somatostatin recep	tachykinin recepto	G protein-coupled	complement C5a ana

ALIGNMENTS

	A39485	
	cransformin	transforming protein (mrg) - human C.Species: Homo saniens (man)
	C; Date: 28-	C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
	R:Monnot, C.; Weber	n: A33463 C.: Weber, V.: Stinnakre, J.; Bihoreau, C.; Teutsch, B.; Corvol, P.; Clauser,
	Mol. Endocr	Mol. Endocrinol. 5, 1477-1487, 1991
	A; Title: Cl A: Reference	A;Title: Cloning and functional characterization of a novel mas-related gene, modulating, A;Reference number: A39485; MUID:92130997; PMID:1723144
	A;Accession: A39485	n: A39485
	A; Status: preliminary	preliminary
	A; Molecule type: DNA	type: DNA
	A; Kesiques:	A;KeBlaueB: 1-3/8 <mun> A;KeBlaueB: 1-3/8 <mun></mun></mun>
	O. Choosefami	TELETITICE D. CHIEFACH.FIJITA (GD.C.COCJ), MID. Selleco, Ann. Chiefach. Co. C. C.C.C.C.C.C.C.C.C.C.C.C.C.C.C.C
·	C; Keywords:	C;Keywords: G protein-coupled receptor; transmembrane protein
	Query Match	tch 26.1%; Score 461; DB 2; Length 378;
	Matches	Matches 107; Conservative 56; Mismatches 81; Indels 38; Gaps 10;
	Q	51 IVSLVALTGNAVVLWLLGCRWRRNAVSIYILNLVAADFLFLSGHIICSPLRLINIR 106
	망	84 LVSLCGVLLNGTVFWLLCCG-ATNPYMVYILHLVAADVIYLCCSAVGFLQVTLLTY 138
	Qy 1	107 HPISKILSPVMTFPYFIGLSMLSALSTERCLSILWPIWYHCRRPRYLSSVMCV 159
	pb 1	139 HGVVFFIPDFLAILSPFSFEVCLCLLVAISTERCVCVLFPIWYRCHRFKYTSNVVCT 195
	0γ 1	160 LUMALSLLRSILEMMFCDFLFSGADSVWCETSDFITIAMLVFLCVVLCGSSLVLL 214
	Db 1	196 LIWGLPFCINIVKSLFLTYWKHVKACVIFLKLSGLFHAILSLVMCVSSLTLL 247
	Ωу 2	215 VRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIF 274
	Db 2	248 IRFLCCSQQQKATKVYAVVQISAPMFLLWALPLSVAPLITDFKMFVTTSYLISLF 302
	Qy 2	275 LSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPEV 316
	Db 3	303 L-IINSSANPITYFFVGSLRKKRLKESLRVILQRALADKPEV 343
	RESULT 2	

transforming protein mas - rat
(;Species: Rattus norvegicus (Norway rat)
(;Species: Rattus norvegicus (Norway rat)
(;Aate: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
(;Aate: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
(;Accession: A31816
(;Accession: A31816
R;Toung, D.; O'Neill, K.; Jessell, T.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 5339-5342, 1988
A;Title: Characterization of the rat mas oncogene and its high-level expression in the h

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Cell 45, 711-719, 1986

A,Title: Isolation and characterization of a new cellular oncogene encoding a protein wi A;Reference number: A01375; MUID:86218084; PMID:3708691

A;Reference number: A01375

A;Reference number: A01375

A;Reference number: A01375

A;Recestion: A01375

A;Rocestion: A01375

A;Residues: 1-325 <YOU>

A;Residues: 1-325 <YOU>

A;Cross-references: UNIPROT:P04201; GB:M13150; NID:g187388; PIDN:AAA36199.1; PID:g307158

C;Genetics:
A;Gene: GB:MAS1

A;Cross-references: UNIPROT:p04201; GB:M13150; NID:g187388; PIDN:AAA36199.1; PID:g307158

C;Genetics:
A;Gene: GB:MAS1

A;Cross-references: GDB:120166; OMIM:165180

A;Map position: 6q24-6q27

C;Superfamily: mas transforming protein

C;Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming prote

F;31-61/Domain: transmembrane #status predicted <TM3>

F;150-172/Domain: transmembrane #status predicted <TM4>

F;150-172/Domain: transmembrane #status predicted <TM5>

F;255-250/Domain: transmembrane #status predicted <TM5>

F;258-286/Domain: transmembrane #status predicted <TM7>

F;58-286/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: A31816; MUID:88276953; PMID:2455902
A;Accession: A31816
A;Molecule type; mRNA
A;Residues: 1-24 <YOU>
A,(Cross-references: UNIPROT:P12526; GB:J03823; NID:g205313; PIDN:AAA41573.1; PID:g205314;
C;Genetics:
A;Gene: mas
C;Guperfamily: mas transforming protein
C;Superfamily: mas transforming protein
C;Superfamily: mas transmembrane #status predicted <TM1>
F;31-47/Domain: transmembrane #status predicted <TM2>
F;149-165/Domain: transmembrane #status predicted <TM4>
F;185-204/Domain: transmembrane #status predicted <TM4>
F;185-204/Domain: transmembrane #status predicted <TM4>
F;225-243/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
C;Accession: A01375
C;Young, D.; Waitches, G.; Birchmeier, C.; Fasano, O.; Wigler, M.
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                       Query Match
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Matches 103
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Matches 108; Conser
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Pred. No. 3.9e
57; Mismatches
                       Score 430.5;
Pred. No. 8.6e
6; Mismatches
                                                8.6e-29
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A; Residues: 1-324 <MET>
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SANPIIYFFVGSFRQRQNRQNLKLVLQRALQD--TPEVDEGGG
                                                                        NTWASHSSKLYIVIMVTIIIFLIFAMPMRVLYLLYYBY---WSA-FGNLHNISLLFSTIN
                                                                                                               GSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALN
                                                                                                                                                              LVTTMEYVMC--IDSGEES--HSRSDCRAVIIFIAILSFLVETPLMLVSSS-ILVVKIRK 215
                                                                                                                                                                                                        LRSILEWMFCDFLFSGADSVWCETSD-----FITI-AWLVFLCVVLCGSSLVLLVRILC 219
                                                                                                                                                                                                                                                    HYTIVTLSVTFLFGYNTGLYLLTAISVERCLSVLYPIWYTSHRPKHQSAFVCALLCALSC
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R;Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnema PBBS Lett. 357, 27-32, 1995
A;Title: Expression of the mouse and rat mas proto-oncogene A;Reference number: I48647; MUID:95094925; PMID:8001672
A;Accession: I48647
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-87,'I', 89-324 <RES>
A;Cross-references: EMBL:X67735; NID:g53011; PIDN:CAA47964.1; PID:g53012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #text_change
C;Date: 10-Apr-1996 #sequence vision 19-Apr-1996 #text_change
C;Accession: S51001; 148647; S29519
R;Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann,
FEBS Lett. 357, 27-32, 1995
A;Title: Expression of the mouse and rat mas proto-oncogene in t
A;Reference number: S51001; MUID:95094925; PMID:8001672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P30554; EMBL:X67735 R;Metzger, R.; Bader, M.; Ludwig, T.; Berberich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Alternate names: mas proto-oncogene protein; probable G protein-coupled receptor
                                                                                                                                                                                                                                                                                                           ;Superfamily: mas transforming protein ;Superfamily: mas transmembrane;Keywords: G protein-coupled receptor; proto-oncogene; transmembrane
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                                                                                                                        52 VSLVALTGNAVVLWLLGCRMRRNAVSIYILNLVAADFLFLSGHIICS-----PLRLINIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SANPIIYFFYGSFRQRQNRQNLKLVLQRALQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSLVALTGNAVVLWLLGCRMRRNAVSIYILNLVAADFLFLSGHIICS-----PLRLINIR 106
HPISKILSPVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRRPRYLSSVMCVLLWALSL 166
                                                                     ISPLGFVENGILLWFLCFRMRRNPFTVYITHLSMADISLLFCIFILSTDYALDYELSSGH 100
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                                                                                                                                                                                        24.3%; Score 428.5; DB 2; 37.7%; Pred. No. 1.3e-28; vative 56; Mismatches 98;
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                                                                                                                                                                                        98;
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Cate 13: Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JQ1231; A46483
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A;Title: Molecular characterization of the interleukin-8 receptor.
A;Reference number: JQ1231; MUID:91378994; PMID:1898400
A;Accession: JQ1231
A;Molecule type: DNA
A;Residues: 1-355 < ABC >
A;Cross-references: UNIPROT:P21109; GB:M74240; NID:g165438; PIDN:AAA31375.1;
A;Cross-references: UNIPROT:P21109; GB:M74240; NID:g165438; PIDN:AAA31375.1;
J. Immunol. 148, 1261-1264, 1992
A;Title: Characterization of complementary DNA clones encoding the rabbit IL
A;Reference number: A46483; MUID:92148149; PMID:1737938
A;Accession: A46483; MUID:92148149; PMID:1737938
A;Accession: A46483; MUID:92148149; PMID:1737938
A;Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A;Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441
A;Cross-reference extracted from NCBI backbone (NCBIN:81526, NCBIP:81530)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G protein-coupled receptor RTA - rat
C;Species: Rattus norvegicus (Norway rat)
C;Apecies: Rattus norvegicus (Norway rat)
C;Accession: A35639
C;Accession: A35639
R;Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.; Lynch, I Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
A;Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue di A;Reference number: A35639; MUID:90222168; PMID:2109324
A;Accession: A35639; MUID:90222168; PMID:2109324
A;Accession: A35639
A;Molecule type: mRNA
A;Residues: 1-343 <ROS>
A;Cross-references: UNIPROT:P23749; GB:M35297; NID:g206809; PIDN:AAA42087.1; PID:g206810
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
C;Keywords: Carbohydrate (Asn) (covalent) #status predicted
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(;species: Oryctolagus cuniculus (domestic rabbit)
C;species: Onar-1992 #sequence_revision 31-Mar-1992
C;Accession: JQ1231; A46483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
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Pred. No. 9e-24
58; Mismatches
                                                                                                                                                                                                                                                                            GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g16543 Wood, W.I.
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                                                                                                                                                                                                                                  the rabbit IL-8 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Mapping of genes for the human C5: A;Reference number: A42009; MUID:92307681; A;Accession: C42009
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C; Accession: C42009
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A;Map position: 19q13.3-19q13.4
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A; Residues: 1-353 < BAO>
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         SGADSVWCET----SDFITIAWLVFLCVVLCGSSLVLLVRILC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLHSCLNPIIYAFIG----QNFRNGFLKMLAARGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALMSSAMPIIYFFVGSFRQRQMRQN--LKLVLQRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                            13.5%; Score 238; DB 2; I
23.8%; Pred. No. 1.4e-12;
ative 76; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.6%; Score 240; DB 2; 27.4%; Pred. No. 9.4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Mismatches 109;
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A;Cross-references: UNIPROT:P25089; GB:M76673; NID:g182668; C;Comment: This fMet-Leu-Phe receptor homolog, whose ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: FMLP-related receptor I; probable chemotactic receptor FPRH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Homo sapiens (man);Date: 30-Sep-1993 #text_change;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L.; Gerard, N.P.; Eddy Jr., R.L.; Shows, T.B.; Gerard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDRYLAIV----HATRTLTQKRHLVKFICLGIWALSLILSLFFFLFRQVFSPNNSSPVC 192
                                              LDRCICVLHPAWAQNHRTMSLAKRVMTGLWIFTIVLTLPNFIFWTTISTTNGDTYCIFNF
                                                                                                                                                                                                  LNLVAADFLFLSGHIICSPLRLINI----RHP----ISKILSPVMTFPYFIGLSMLSAIS 132
                                                                                                                                                                                                                                                                                                    PINGREE-----TPCYKOTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNAVSIYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TERCLSILWPIWYHCRR----PRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YILNLVAADFLFLSGHIICSPLRLIN-----IRHPISKILSPVMTFPYFIGLSMLSAIS 132
                                                                                              TERCLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMF---
                                                                                                                                                  LNLALADFSFSA----ILPFRMVSVAMREKWPFASFLCKLVHVMIDINLFVSVYLITIIA 120
                                                                                                                                                                                                                                                      PLNETEEVLPEPAGHTVLWIFSLLVHGVTFVFGVL---GNGLVIWVAGFRMTRTVNTICY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLVFLLCGLPFGIQWALFSRIHLDWKVLFC----HVHLV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEDLGHNTAKWRMVLRILPHTFGFILPLLVMLFCYGFTLRTLFQAHMGQKHRAMRVIFAV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGMPPVE-KDYSPCLVVTQTLNKYVVVVIYALVFLLSLLGNSLVMLVILYSRSNRSVTDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ETSDFITIAWLVFLCVV--LCGSSLVLLVRILC-GSRKMPLTRLYV-----TILLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-coupled receptor; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLLADTLMRTHVIQETCQRRNDIDRALDATEILG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor (C5AR),
                                                                                                                                                                                                                                                                                                                                                                                                        Length 353
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interleukin-8 receptor, high affinity - rabbit
N;Alternate names: fMLP receptor
C;Bpecies: Oryctolagus cuniculus (domestic rabbit)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A23669
R;Thomas, K.M.; Pyun, H.Y.; Navarro, J.
J. Biol. Chem. 265, 20061-20064, 1990
J. Biol. Chem. 265, 20061-20064, 1990
A;Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.
A;Reference number: A23669; MUJD:91056034; PMID:1700779
A;Accession: A23669
A;Molecule type: mRNA
A;Residues: 1-354 <THO>
A;Residues: 1-354 <THO>
A;Residues: 1-354 <THO>
A;Cross-references: UNIPROT:P21109; GB:M58021; GB:J05705; NID:g165442; PIDN:AAA31377.1;
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil
                                                                                                 C/Species: Homo sapiens (man)
C/Species: Homo sapiens (man)
C;Date: 07-Oct.1994 #sequence revision 12-Apr-1996 #text_change
C;Accession: 137898; 138712; Ā53611; A39446
R;Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A;Title: Comparison of the genomic organization and promoter fun
A;Reference number: 137898; MUID:95014476; PMID:7929358
  A; Cross-references:
                      A;Accession: I37898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <RES>
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                                                                                                                                                                                                                                                             interleukin-8 receptor type B - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELTPINGREETPC--YKQTLS---FTGLTCIVSLVALTGNA-VVLWLLGCRMRRNAVSI
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                                                                                                                                                                                                                                                                                                                                                                     AFIG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SR--PL-RVFAAV---VASFFICWFPYELIGILMAVWLKEMLLNGKYKIILVLINPTS-S 289
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  UNIPROT: P25025; EMBL: U11869; NID: g511801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.4%; Score 235.5; DB 2; 28.9%; Pred. No. 2.2e-12; tive 53; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIY 287
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    PIDN: AAB60656.1;
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    PID:95118
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                                         A;Reference number: A53752;
A;Accession: A53752
A;Status: preliminary
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A; Residues: 6-360 cMVR>
A; Cross-references: GB:M72
C; Comment: This receptor,
C; Genetics:
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A; Residues: 6-360 <SPR>
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Best Local
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A;Map position: 2q35-2q35
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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Science 253, 1280-1283, 1991
A;Title: Cloning of complementary DNA encoding a functional human interleukin-8 receptor
A;Reference number: A39446; MUID:91368200; PMID:1891716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-15 <REZ-
A;Residues: 1-15 <REZ-
A;Cross-references: EMEL:U11872; NID:g511808; PIDN:AAA64380.1; PID:g511809; EMBL:U11873;
A;Cross-references: EMEL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID
11876; NID:g511816; PID:g511817; EMBL:U11877; NID:g511818; PID:g511819; EMBL:U11878; NID
R;Sprenger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A;Title: Structure, genomic organization, and expression of the human interleukin-8 received approximate the structure of the h
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A;Cross-references: GDB:127868; OMIM:146928
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A;Status: preliminary; nucleic
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A;Status: prelimina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 VDRYLAIV-----HATRTLTQKRYLVKFICLSIWGLSLLLALPVLLFRRTVYSSNVSPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 EETPCYKQTLSFTG-----LTCIVSLVALTGNA-VVLWLLGCRMRRNAVSIYILNLVAAD
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Similarity 26.3%; Pred. No. 1.3e-11;
82; Conservative 52; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAAPCEPESLEINKYFVVIIYALVFLLSLIGNSLVMLVILYSRVGRSVTDVYLLNLALAD 94
                                                                                                                         PIIYFFVG-SFR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TERCLSILWPIWYHCRR----PRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLF------LSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAIS 132
                                                                                                                                                                                                                                                                                                                                                                      VLVFLLCGLPFG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEDMGNNTANWRMLLRILPQSFGFIVPLLIMLFCYGFTLRTLFKAHMGQKHRAMRVIFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ETSDFITIAWLVFLCVV--LCGSSLVLLVRILC-GSRKMPLTRLYV-----TILLT 236
PLIYAFIGOKFR
                                                                                                                                                                                                                                                   VLIFILCWLPYNLVLLADTLMRTQVIQETCERRNHIDRALDATEI - - -
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      322
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                                                                                                                                                                                                                                                                                                                                                                -IQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSAN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             several peptides besides interleukin-8, inc
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isotype E.; Navarro

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R; Yamada, Y; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
A; Title: Cloning and functional characterization of a family of human and mouse somatost A; Feference number: A41795, MUID:92108031; PMID:1346068
A; Accession: D41795
A; Status: nucleic acid sequence not shown
A; Wolecule type: DNA
A; Residues: 1-369 < YAM'
A; Residues: 1-369 < YAM'
A; Cross-references: UNIPROT:P30875; GB:M81832; NID:9201060; PIDN:AAA58256.1; PID:9201061
R; Blliott, D.B.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.V.
J. Immunol. 153, 1180-1186, 1994
A; Title: T lymphocytes isolated from the hepatic granulomas of schistosome-infected mice A; Reference number: 156236; MUID:94300079; PMID:7913111
A; Molecule type: mRNA
A; Residues: 99-309 < RES'
A; Cross-references: GB:S71756; NID:9560631
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      somatostatin receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D41795; I56236
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A;Residues: 1-358 <PRA>
A;Residues: 1-358 <PRA>
A;Cross-references: UNIPROT: p35344; GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g43766:
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein
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Best Local 9
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YILNLAIADELFMLG-LPFLAMQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSID
                                              YILNLVAADFLFLSGHIICSPLRLINIRHPISK-ILSPVMT----PPYFIGLSMLSAISTE 134
                                                                                                                                              LGTELTPINGREET-PCYKQTLS--FTGLTCIVSLVALTGNAVVLW-LLGCRMRRNAVSI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSCLNPITYAFIGOKFR
                                                                                                     LNGSLGPSNGSNQTEPYYDMTSNAVLTFIYFVVCVVGLCGNTLVIYVILRYAKMKTITNI
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Pred. No. 4.5e-11;
                                                                                                                                                                                                                            Score 219.5; DB 2; Pred. No. 5.1e-11;
                                                                                                                                                                                                     Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112; Indels
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                                                                                                                                                                                                     Indels
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  RASSULT 13
B42009
FMLP-related receptor 1 - human
N;Alternate names: FMLP receptor homolog FPR2; formyl peptide receptor like-1;
C;Species: Homo sapiens (man)
C;Date: 30-Sep_193 #sequence revision 14-Jul-1995 #text change 09-Jul-2004
C;Accession: B42009; JCl258; JQ1521; A42492; I54751; S21581
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A;Cross-references: UNIPROT:P30680; GB:M93273; NID:g207026; PIDN:AAA42165.1; A;Note: sequence extracted from NCBI backbone (NCBIN:102315, NCBIP:102316) C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kluxen, F.W.; Bruns, C.; Lubbert, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 4618-4622, 1992
A;Title: Rxpression cloning of a rat brain somatostatin
A;Reference number: A45291; MUID:92262491; PMID:1374909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-369 < KLU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              somatostatin receptor, somatotropin release-inhibiting factor receptor, Cispecies: Rattus norvegicus (Norway rat)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INWPGESGAW--YTGFIIYAFILGFLVPLTIICLCYLFIIIKVKSSGIRVGSSKRKKSEK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYLAVVHPIKSAKW---RRPR-TAKMINVAVWCVSLL-VILPIMIYAGLRSNQWGRSSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCLSILWPI----WYHCRRPRYLSSVMCVLLWALSLLRSILEWMF---
ANPILYAFLSDNFKKSFQNVLCLVKVSGAEDGERSD
                                    ANPITYFFVGSFRQRQNRQNLKLVLQRALQDTPEVD
                                                                              KVTRMVSIVVAVPIFCWLPFYIFNVSSVSVAISPTPAL--KGMFDFV----VILTYANSC
                                                                                                                   YVT--ILLTVLVFLLCGLPF-----GIQWALFSRIHLDWKVLFCHVHLVSIFLSALNSS 281
                                                                                                                                                                                              FLFSGADSVWCETSDFITIAWLVFLCV---VLCGSSLVLLVR-----ILCGSRKMPLTRL 229
                                                                                                                                                                                                                                        RYLAVVHPIKSAKW---RRPR-TAKMINVAVWGVSLL-VILPIMIYAGLRSNOWGRSSCT
                                                                                                                                                                                                                                                                        RCLSILWPI----WYHCRRPRYLSSVMCYLLWALSLLRSILEWMF------CD 177
                                                                                                                                                                                                                                                                                                                    YILMLAIADELFMLG-LPFLAMQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSID 139
                                                                                                                                                                                                                                                                                                                                                         YILMLVAADFLFLSGHIICSPLRLINIRHPISK-ILSPVMT---FPYFIGLSMLSAISTE 134
                                                                                                                                                                                                                                                                                                                                                                                                  LNGSLGPSNGSNQTEPYYDMTSNAVLTFIYFVVCVVGLCGNTLVIYVILRYAKMKTITNI 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANPILYAFLSDNFKKSFQNVLCLVKVSGTEDGERSD
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Pred. No. 5.1e
55; Mismatches
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Genomics 13, 437, 440, 1992
Artill: Mapping of genes for the human (5% receptor (GAR), human PRLP receptor (FPR), Artill: Mapping of genes for the human (5% receptor (GAR), human PRLP receptor (FPR), Artill: Mapping of genes for the homon (All Color)
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Similarity
                                                                               12.3%;
ilarity 25.7%;
Conservative 60
                                                                               60;
                                                                               Score 217; DB
Pred. No. 7.9e-
0; Mismatches
                                                                                                                                   Length 351;
                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-346 <VAN>
A;Cross-references: UNIPROT:P30875; EMBL:X68951; NID:g54197; PIDN:CAA48766.1; PID:g54198
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Cloning and expression of a novel mouse somatostatin A;Reference number: S29248; MUID:93012001; PMID:1397330 A;Accession: S29248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Vanetti, M.; Kouba, M.; Wang, X.; Vogt, FEBS Lett. 311, 290-294, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Mus musculus (house mouse)
;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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Best Local Similarity
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307
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                                                                                                                                                                                                                                                                                                                                                     81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STERCLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMF------CDFL 179
                                         ANPIIYFFVGSFRQRQNRQNLKLVLQRAL
                                                                                                                                                                            INWPGESGAW--YTGFIIYAFILGFLVPLTIICLCYLFIIIKVKSSGIRVGSSKRKKSEK 252
                                                                                                                                                                                                                                                                                                          RCLSILWPI----WYHCRRPRYLSSVMCVLLWALSLLRSILEWMF-----
                                                                                                                                                                                                                                                                                                                                                                                               YILNLVAADFLFLSGHIICSPLRLINIRHPISK-ILSPVMT---FPYFIGLSMLSAISTE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGTELTPINGREET-PCYKQTLS--FTGLTCIVSLVALTGNAVVLW-LLGCRMRRNAVSI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSSLAFFNSCLNPMLYVFVGQDFRERL-IHSLPTSLERALSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSRKMPLTRLYVTILLTVLV--FLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALDRCICVLHPVWAQNHRTVSLAMKVIVGPWILALVLTLPVFLFLTTVTIPNGDTYCTFN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLNLALADFSFTA----TLPFLIVSMAMGEKWPFGWFLCKLIHIVVDINLFGSVFLIGFI 119
                                                                                    KVTRMVSIVVAVFIFCWLPFYIFNVSSVSVAISPTPAL--KGMFDFV----VILTYANTC 306
                                                                                                                              YVT--ILLTVLVFLLCGLPF-----GIQWALFSRIHLDWKVLFCHVHLVSIFLSALNSS 281
                                                                                                                                                                                                                   FLFSGADSVWCETSDFITIAWLVFLCV---VLCGSSLVLLVR-----ILCGSRKMPLTRL 229
                                                                                                                                                                                                                                                              RYLAVVHPIKSAKW---RRPR-TAKMINVAVWCVSLL-VILPIMLYAGLRSNQWGRSSCT 194
                                                                                                                                                                                                                                                                                                                                                     YILNLAIADELFMLG-LPFLAMQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSID 139
                                                                                                                                                                                                                                                                                                                                                                                                                                          LNGSLGPSNGSNQTEPYYDMTSNAVLTFIYFVVCVVGLCGNTLVIYVILRYAKMKTITNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSGADSVWCETSD---FITIAWLVFLCVV--LCGSSLVLLVRILC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPLNEYEEVS--YESAGYTVLR-ILPLVVLGVTFVLGVLGNGLVIWVAGFRMTRTVTTIC
ANPILYAFLS --
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-DNFKKSFQNVL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 214.5; DB 2
Pred. No. 1.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
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                                                                                                                                                                                                                                                                                                            CD 177
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15

receptor

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A;Cross-references: GDB:202662; OMIM:182454
A;Map position: 20p11.2-20p11.2
A;Map position: 20p11.2-20p11.2
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phd
c;47-73/Domain: transmembrane #status predicted <TM1>
F;84-109/Domain: transmembrane #status predicted <TM3>
F;121-142/Domain: transmembrane #status predicted <TM4>
F;2208-238/Domain: transmembrane #status predicted <TM6>
F;257-284/Domain: transmembrane #status predicted <TM6>
F;257-284/Domain: transmembrane #status predicted <TM7>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-198/Disulfide bonds: #status predicted
F;119-198/Disulfide bonds: #status predicted
F;111-253/Binding site: phosphate (Ser) (covalent) #status predicted
F;1327/Binding site: palmitate (Cys) (covalent) #status predicted
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A;Residues: 1-82,'T',84-364,'K',366-388 <ROH>
A;Residues: 1-82,'T',84-364,'K',366-388 <ROH>
A;Cross-references: GB:L07833; NID:g307429; PIDN:AAA60565.1; PID:g307430
A;Kote: sequence extracted from NCBI backbone (NCBIN:130856, NCBIP:130858)
C;Comment: This protein mediates the diverse actions of the tetradecaptide somatostatin.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P31391, GB:L14856; NID:g292499; PIDN:AAA36623.1; PID:g292500 R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A;Title: Cloning, functional expression and pharmacological characterization of a fourth A;Reference number: JN0762; MUID:93384611; PMID:8373420
A;Accession: JN0762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:D16826; NID:g693907; PIDN:BAA04106.1; PID:g693908 R;Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R. Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993 A;Title: Cloning and characterization of a fourth human somatostatin receptor. A;Reference number: A47457; MUID:93248256; PMID:8483934 A;Accession: A47457
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A;Molecule type: DNA
A;Residues: 1-388 <XUY>
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C;Darcies: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JN6605; JN9762; Ā47457
R;Xu, Y:; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A;Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A;Reference number: JN0605; MUID:93290656; PMID:8512564
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Residues: 1-388 <YAM>
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270 LVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPEVDEGGGWLPQETLE 329
                                                                             238 MRAVALRAGWQQRRRSEKKITRLVLMVVVVFVLCWMPFYV----VQLLNLVVTSLDATVN 293
                                                                                                                                                           210 SLVLLVRILCGSRKMPLTRLYVTILLTVLVPLLCGLPPGIQWALFSRIHLDWKVLFCHVH 269
                                                                                                                                                                                                                                         178 TLPIAIFADTRPARGGQAVACNLQWPHPAWSAVFVVYTFLLGFLLPVLAIGLCYLLIVGK 237
                                                                                                                                                                                                                                                                                                                   169 SILEWMFCDFL-FSGADSVWCB-----TSDFITIAWLV----FLCVVLC----GS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 LS----PVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRRPRYLSSVMCVLLWALSLLR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GLVGNALVIFVILRYAKMKTATNIYLLNLAVADELFMLSVPFVASSAAL---RHWPFGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 ALTGNAVVLW-LLGCRMRRNAVSIYILNLVAADFLF-LSGHIICSPLRLINIRH-PISKI 112
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Db 294 HYSLILSYANSCANPILYGFLS-----DNFRRSFQRVLCLRCCLLEGAGGABEEPLD 345

Oy 330 LSGSRLE 336

Db 346 YYATALK 352
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Search completed: October 27, 2004, 08:35:03
Job time: 40 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                     UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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1763
1 MESKSSWVIRLGFLSNDSTI......EGGGWLPQETLELSGSRLEQ 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                  SUMMARIES
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5 4	Score	Query Match	Query Match Length DB	₩	ID	Description
۲	1688	95.7	322	- :	MRG3_HUMAN	Q961b0 homo sapien
N	1663	94.3	322	N		2 hon
w	1606	91.1	322		SNS2_HUMAN	Q8tde0 homo sapien
4	1411	80.0	322	_	SNS3_HUMAN	homo
σ	1383	78.4	322	_	MRG1_HUMAN	homo
σ	1382	78.4	322	Н	SNS5_HUMAN	homo
7	1367	77.5	322	_	MRG4 HUMAN	homo
8	989.5	56.1	330	_	MRG2 HUMAN	homo
9	989.5	56.1	330	N	AAH63450	Aah63450 homo sapi
6	823.5	46.7	323	N	Q7TN42	Q7tn42 rattus norv
Ξ	820.5	46.5	323	щ	SNS1_RAT	Q8r4g1 rattus norv
2	797	45.2	322	N	Q8CIP3	Q8cip3 mus musculu
ü	782	44.4	304	,_	MRGA_RAT	
4	778	44.1	331	N	Q91YB7	Q91yb7 rattus norv
5	763	43.3	338	N	Q8CDY4	Q8cdy4 mus musculu
6	763	43.3	338	N	Q91ZC2	
7	761	43.2	304	Ъ	MGA1_MOUSE	Q91ww5 mus musculu
8	754	42.8	294	N	Q7TN48	Q7tn48 rattus norv
6	739.5	41.9	301	_	MGA6_MOUSE	Q91zc6 mus musculu
8	729	41.3	302	-	MGA3_MOUSE	Q91ww3 mus musculu
21	722.5	41.0	305	μ,	MGA7_MOUSE	Q91zc5 mus musculu
22	713	40.4	321	N	Q91ZC0	Q91zc0 mus musculu
23	703	39.9	338	N	Q91ZC3	Q91zc3 mus musculu
24	691.5	39.2	313	۲,	MGA4 MOUSE	Q91ww2 mus musculu
25	682.5	38.7	331	N	AAH64040	Aah64040 mus muscu
8	681.5	38.7	323	N	Q7TN45	Q7tn45 rattus norv
27	680.5	38.6	305	_	MGA2 MOUSE	Q91ww4 mus musculu
28	680	38.6	304	_	MGA5_MOUSE	Bru
8	674	38.2	322	N	Q91ZB9	Britt
ö	669.5	38.0	305	۳	MGA8 MOUSE	Q91zc4 mus musculu
3	638	36.2	314	N	Q7TN47	Q7tn47 rattus norv

626.5 35.6 31.2 Q7TNA4 617.5 35.0 31.2 Q7TNA4 617.5 33.8 328 2 Q7TNS0 578.5 32.8 245 2 Q7TNA3 578.5 32.7 247 2 Q7TNA6 568.5 32.7 247 2 Q7TNA6 568.5 32.7 320 1 MRGD_MACFA 541.5 30.7 320 1 MRGD_HUMAN 506 28.7 321 1 MRGD_HUMAN 506 28.7 321 2 AAR05120 506 28.7 321 2 BAD20638 503 28.5 310 2 Q7LIF 503 28.5 310 2 Q7LB7 503 28.5 310 2 Q7LB7 503 28.5 310 2 CAC86257
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Q7TM44 Q91ZC1 Q91ZC1 Q7TM50 Q7TM43 Q7TM46 Q7TM51 MRGD MACFA BAD27641 MRGD HUMAN ARROS120 BAD20638 Q71119 Q91ZB7 Q91ZB7 Q91ZB7

ALIGNMENTS

RA Diatchenko L., Marusi RA Diatchenko L., Marusi RA Stapleton M., Soares RA Brownstein M.J. Usel RA Raha S.S., Loquellano RA Raha S.S., McEwan P. RA Richards S., Worley K. RA Villalan D.K., Muzny RA Whiting M., Madan A., RA Whiting M., Madan A., RA Blakesley R.W., Touch RA Rodriguez A.C., Grinw RA Butterfield Y.S.N., X RA Butterfield Y.S.N., X RA Schnerch A., Schein J RT "Generation and initi		MEG3_HUMAN STANDARD AC Q96LBO; Q8TDE1; DT 01-OCT-2004 (Rel. 45, L DE Mass-related G-protein coup geoific G-protein coup gName=MRCX3; Synonyms=SN GN Homo sapiens (Human). Bukaryota; Metazoa; Cho OC Mammalia; Eutheria; Pri OX NCBL_TaxID=9606; RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=21435808; PubMe RA Dong X., Han SK., Zyl RT nociceptive sensory neu RL Cell 106:619-632(2001).
Diatchenko L., Marusina K., Farmer A.A., Rubii Diatchenko L., Marusina K., Farmer A.A., Rubii Stapleton M.J., Usdin T.B., Bonaldo M.F., Casai Brownstein M.J., Usdin T.B., Toshiyuki S., Casai Raha S.S., Loquellano N.A., Peters G.J., Abrar Bosak S.A., McEwan P.J., McKernan K.J., Malek Richards S., Worley K.C., Hale S., Garcia A.M. Villalon D.K., Muzny D.M., Sodergren B.J., Lu Fahey J., Helton E., Ketteman M., Madan A., Ru Whitling M., Madan A., Young A.C., Shevchenko Blakesley R.W., Touchman J.W., Green B.D., Dic Rodriguez A.C., Grimwood J., Schmutz J., Myeri Butterfield Y.S.N., Krzywinski M.I., Skalska Schnerch A., Schein J.E., Jones S.J.M., Marka Schnerch and initial analysis of more than and mouse cDNA sequences.";	[2] SEQUENCE FROM N.A., VARIANT ASN-169, AND MEDLINE=21853733; PubMed=11850634; DOI=10 MEDLINE=21853733; PubMed=11850634; DOI=10 Lembo P.M.C., Grazzini E., Groblewski T., Zhang J., Hoffert C., Cao J., Schmidt R., Gosselin M., Fortin Y., Banville D., Shen Dray A., Walker P., Ahmad S.; "Proenkephalin A gene products activate a neuron-specific GPCRs."; Nat. Neurosci. 5:201-209(2002). [3] SEQUENCE FROM N.A. TISSUB=Testis; MEDLINE=2388257; PubMed=12477932; DOI=10 Strausberg R.E., Feingold E.A., Grouse L. Klausner R.D., Collins F.S., Wagner L., S Altschul S.F., Zeeberg B., Buetow K.H., S Altschul S.F., Jordan H., Moore T., Max S.	DARD; 5, Created) 5, Last sec 5, Last and in coupled recoupled rec
Casavant T.L. Casavant T.L. Casavant T.L. Casavant T.P. Ca	TISSUE SPECII .1038/nn815; O'Donnell D. Pelletier M. S., Stroem i new family o	ce update) tion update) eptor member X3 (Se or 1). niata; Vertebrata; arrhini; Hominidae; imon M.I., Anderson sed in specific sub
Hong L. Scheetz T.E., Prange C. Prange C. Mullahy S.J., hunaratne P.H., J., Hulyk S.W., bs R.A., S., Sanchez A., fard G.G., C., C., lus D.E., lus D.E., full-length human	ROY MO., Labbarre M., Labbarre M., Payza K., Stensory Schuler G.D., Schuler G.D., Shat N.K., Hsieh F.,	nsory neuron- Buteleostomi; Homo.

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Pfam; pF00001; 7tm 1;

Pfam; pF00001; 7tm 1;

PRINTS; pR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G-PROTEIN ECEP F1 2; 1.

PROSITE; pS50262; G-PROTEIN POlymorphism; Transmembrane.

Extracellular (Potential).

**Contential**

**Contential*

**Content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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PUNCTION: Orphan receptor. Probably involved in the function of process of the function and/or nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Potently activated by enkephalins (By similarity).

SUBCELIULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeninal sensory neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         root and trigeminal sensury neurons.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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                                                                                                                                                                                       CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                                                                                                                                                                                                             CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                                                                                                                                                                                                                                                                                             VSIYILMLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
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RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                                                IAWLVFLCVVLCGSSLVLLVRILCGSRKWPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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/FTId=VAR 0.19434.
S -> P (in Ref. 2).
C -> R (in Ref. 3).
W -> Q (in Ref. 3).
R -> K (in Ref. 2).
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KIAUSHER Z. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

KIAUSHER R.F., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Wullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Woorley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R. W., Touchman J.W., Green E.D., Dickson M.C.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
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AAH67292;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; BC067292; AAH67292.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-coupled receptor MRGX3.
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                 IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
                                                                                          CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
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                                                                     CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequences.";
l. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                   322 AA;
                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 7.9e-114;
0; Mismatches 2;
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LT 3
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Q8TDE0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a centre of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815; Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Dray A., Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Sensory neuron-specific G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF474988; AAL86879.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=SNSR2;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Proenkephalin A gene products activate a new neuron-specific GPCRs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nociceptive neurons. May regulate nociceptor function development, including the sensation or modulation of Potently activated by enkephalins (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: Uniquely localized in a subset of root and trigeminal sensory neurons.

SIMILARITY: Belongs to family 1 of G-protein coupled r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurosci. 5:201-209(2002).
FUNCTION: Orphan receptor. Probably involved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an email to license@isb-sib.ch).
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Primates;
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RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                              Transmembrane.
Extracellular (Potential).
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2 (Potential
                               Extracellular (Potential) 7 (Potential).
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                                                                                                                        nociceptive neurons. May regulate nociceptor function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Potently activated by enkephalins including BAM22 (bovine adrenal medulla peptide 22) and BAM (8-22). BAM22 is the most potent compound and evoked a large and dose-dependent release of intracellular calcium in stably transfected cells. G(alpha)q proteins are involved in the calcium-signaling pathway.

-I- SUBCELIULAR LOCATION: Integral membrane protein.
-I- TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeninal sensory neurons.
-I- SIMILARITY: Belongs to family 1 of --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
SEQUENCE -
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01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Sensory neuron-specific G-protein coupled rec
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Gosselin M., Fortin Y., Banville
Dray A., Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                                                                                                                  "Proenkephalin A gene products activate a new neuron-specific GPCRs.";
Nat. Neurosci. 5:201-209(2002).
-i- FUNCTION: Orphan receptor. Probably involv
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Mammalia; Eutheria;
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..2e-109;
hes 9;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

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Best Local S
Matches 272
                    E Mas-related G-protein coupled receptor 4).

Sepecific G-protein coupled receptor 4).

Name=MKGX1; Synonyms-SNSR4;
Homo sapiens (Human).

Eukaryota; Meranan
                                                                                                                      HUMAN
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DOMAIN
Mammalla; Eutheria; Primates; NCBI_TaxID=9606; [1]
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrane.

DOMAIN 1 31 Extracellular (Potential).
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Pfam; PF00001; 7tm_l; 1.
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Extracellular (Potential).

3 (Potential).

Cytoplasmic (Potential).

4 (Potential).

Extracellular (Potential).

5 (Potential).

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Cytoplasmic (Potential).

6 (Potential).

Extracellular (Potential).

7 (Potential).
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Pred. No. 2.2e-95;
6; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (P
4C43E33E52DCBFF5 CRC64;
                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;
Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D.,
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M.,
Gosselin M., Fortin Y., Banville D., Shen S., Stroem P.,
Dray A., Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor genes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
-i- FUNCTION: Orphan receptor. Probably involv
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MEDLINE=21435808; PubMed=11551509;

Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson

"A diverse family of GPCRs expressed in specific subs

nociceptive sensory neurons.";

Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome sequence."
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"Identification of G
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Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 520:97-101(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Potently activated by enkephalins including BAM22 (bovine adrenal medulla peptide 22) and BAM (8-22). BAM22 is the most potent compound and evoked a large and dose-dependent release of intracellular calcium in stably transfected cells. G(alpha)q proteins are involved in the calcium-signaling pathway. SUBCELULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeminal sensory neurons.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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G protein-coupled
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Labarre M.
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   "" "Proenkephalin A gene products activate a new family of reuron-specific GPCRs." "Nat. Neurosci. 5:201-209(2002).

"I "PUNCTION: Orphan receptor. Probably involved in the financiceptive neurons. May regulate nociceptor function development, including the sensation or modulation of Potently activated by enkephalins (By similarity).

"I SUBCELLULAR LOCATION: Integral membrane protein.
"TISSUE SPECIFICITY: Uniquely localized in a subset of root and trigeminal sensory neurons.

"Has subfamily"
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Best Local Similarity
Matches 269; Conserv
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Q8TDD7;
01-OCT-2004
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                                                                                                                                                        SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

MEDILINE=21853733; PubMed=11850634; DOI=10.1038/nn815;

Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D.,

Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M.,

Gosselin M., Fortin Y., Banville D., Shen S., Stroem P.,

Dray A., Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                          01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last amoutation update)
Sensory neuron-specific G-protein coupled receptor
                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                              Name=SNSR5;
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6 (Potential).
Extracellular (Potential)
7 (Potential).
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I -> V (in Ref. 2
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Labarre M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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PROSITE; PS00237; G PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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TMRG4 HUMAN STANDARD; PRT; 322 AA. 095LA9; Q8TDD6; O1-OCT-2004 (Rel. 45, Created) O1-OCT-2004 (Rel. 45, Last sequence update) O1-OCT-2004 (Rel. 45, Last annotation update) Mas-related G-protein coupled receptor member specific G-protein coupled receptor 6).

Name=NRGX4; Synonyms=SNSR6;

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(Sensory

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InterPro; IPKUUULII, 1.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR000217; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP
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MEDLINE-2185373; FubMed=11850634; DOI=10.1038/nn815;

Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Roy M.-O.,

Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Labarre M.,

Gosselin M., Fortin Y., Banville D., Shen S., Stroem P., Payza K.,

Dray A., Walker P., Ahmad S.;

"Proenkephalin A gene products activate a new family of sensory

neuron-specific GPCRS.";
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Dong X., Han S.-K., Zylka M.J., Simon
"A diverse family of GPCRs expressed i
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeminal sensory neurons.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collat ween the Swiss Institute of Bioinformatics and the EMBL outst Buropean Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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/FTId=VAR 019436.

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S -> L (in dbsNp:1869788).

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A -> V (in Ref. 2).
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N-linked (GlcNAc...)
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N-> K (in dbSNP:2445180).
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01-OCT-2004 (Rel. 4
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Tsutsumi
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Dong X., Han S.-K., Zylka M.J., Simon M.I.,
"A diverse family of GPCRs expressed in spec
nociceptive sensory neurons.";
Cell 106:619-632(2001).
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MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
                                                           TISSUE=Brain;
MEDLINE=22388257;
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"Genome-wide discovery
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atani H., Asai K., Akiyama
overy and analysis of humar
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerach A., Schein J.E., Jones S.J.M., Marra M.A.;
RT and mouse cDNA sequences.";
Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRHADDSN.

PROSITE; PS00237; GFROTEIN RECEP F1 2; 1.

PROSITE; PS0262; G_PROTEIN_RECEP F1 2; 1.

PROSITE; PS0262; G_PROTEIN_RECEP F1 2; 1.

PROMAIN

1 33 Extracellular (Potential).

TRANSMEM 34 54 (Potential).

TRANSMEM 64 84 2 (Potential).

TRANSMEM 95 96 Extracellular (Potential).

TRANSMEM 97 117 3 (Potential).

TRANSMEM 118 144 Cytoplasmic (Potential).

TRANSMEM 145 165 4 (Potential).

DOWAIN 118 144 Cytoplasmic (Potential).

TRANSMEM 145 165 4 (Potential).

DOWAIN 166 184 Extracellular (Potential).

TRANSMEM 185 205 205 5 (Potential).

TRANSMEM 185 205 5 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/amor send an email to license@isb-sib.ch).
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J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY042214; AAK91805 1; -.
EMBL; AD083626; BAB89339.1; -.
EMBL; AB065811; BAC06030.1; -.
EMBL; BC063450; AAH63450.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "MrgX2
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SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Has a limited expression profile, be peripheral and within the central nervous system, with levels in dorsal root ganglion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sleep regulation locomotor activity, and corrical function. In receptor-expressing cells, cortistatin-stimulated increases in intracellular \text{Ca}(2+) but had no effect on basal or forskolinstimulated cAMP levels, suggesting that this receptor is G(q)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mas subfamily.
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l. Acad. Sci. U.S.A. 99:16899-16903(2002)
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RA Strausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiteh F., RA Linkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsiteh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Pillalon D.K., Young A.C., Shevchenko Y., Bouffard G.G., RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Fahey J., Hall R., Young A.C., Shevchenko Y., Bouffard G.G., RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schein J.E., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Jones S.J., Marra M.A.; Schmutz J., Myers R.M., Butterfield Y.S., RA Jones S.J., Marra M.A.; Schmutz J., Marra M.A.; Schein J.E., RT Tenderation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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AAH63450;
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Pred. No. 1.5e-64;
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N -> S (in dbSNP:10833049)
/FTId=VAR_019433.
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AC Q7TN4
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K MEDLINE=22810130; PubMed=12909716;

A Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;

A Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;

T Proc. Natl Acad Sci. U.S.A. 100:10043-10048 (2003).

Proc. Natl Acad Sci. U.S.A. 100:10043-10048 (2003).

R EMBL; AF518245; AAQ08317.1;

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004772; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001786; P:G-protein coupled receptor protein signalin.

InterPro; IPR000276; GPCR_Rhodpsn.
Query Match
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Matches 172
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Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                Q7TN42;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
MRGC G protein-coupled receptor.
Name=Mrgc;
                                                                                    Pfam; PF00001; 7tm 1; 1.

PROSITE; PS00237; G PROTEIN RECEP_F1_1;

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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62.1%; Pred. No. 1.56
tive 27; Mismatches
46.7%; Score 823.5;
52.8%; Pred. No. 2.1:
ive 51; Mismatches
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OBR4G1;
O1-OCT-2004 (Rel. 45, Created)
O1-OCT-2004 (Rel. 45, Last sequence update)
O1-OCT-2004 (Rel. 45, Last annotation update)
Sensory neuron-specific G-protein coupled receptor
                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entities requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                               Nat. Neurosci. 5:201-209 (2002).

Nat. Neurosci. 5:201-209 (2002).

PUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain.

Potently activated by enkephalins (By similarity).

Potently activated by enkephalins (By similarity).

SUBCELIULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Uniquely localized in a subset of small dor root and trigeminal sensory neurons. Associated preferentially with 184 class of small-diameter somatosensory afferents (also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lembo P.M.C., Grazzini E., Groblewski T.,
Zhang J., Hoffert C., Cao J., Schmidt R.,
Gosselin M., Portin Y., Banville D., Shen
Dray A., Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
STRAIN-Sprague-Dawley;
MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;
                                 EMBL; AF474986; AAL86877.2; ALT_INIT
                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Proenkephalin A gene products activate a new neuron-specific GPCRs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Snsr1; Synonyms=Snsr; Rattus norvegicus (Rat).
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SIMILARITY: Belongs to
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                  Sner1.
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                                                                                        (See http://www.isb-sib.ch/announce/
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n S., Stroem P.,
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Q8CIP3;
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
G protein-coupled recepto
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI TaxID=10090;
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STRAIN=C57BL/6; MEDLINE=22317401; PubMed=12397184; MEDLINE=22317401; PubMed=12397184; Han S.K., Dong X., Hwang J.I., Zylka M.J., Anderson D.J., Simon M.I.; "Orphan G protein-coupled receptors MrgA1 and MrgC11 are distinctively activated by RF-amide-related peptides through the Galpha q/11 pathway.";
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PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                      SEQUENCE FROM N.A.
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BLrel. 23, Last sequence update)
BLrel. 26, Last annotation updat
receptor MrgCll.
                                                                                                                                                                                                                                                    Chordata;
Rodentia;
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Extracellular (Potential).
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
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Extracellular (Potential).
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8 Extracellular (Potential).
7 (Potential).
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Pred. No. 3.4e
51; Mismatches
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N-linked
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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1es 93;
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Best Local S
Matches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LT 13
                                                        STRAIN=Sprague-Dawley;

MEDLINB=22810130; PubMed=12909716; DOI=10.1073/pnas.1732949100;

Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;

Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;

"Atypical expansion in mice of the sensory neuron-specific Mrg

protein-coupled receptor family.";

Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simon M.I.;

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databas EMBL; AY152435; AAN64385.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; I

GO; GO:0001584; F:rhodopsin-like receptor protein
                                                                                                                                                                                                                                                                                                                                                         OTIN49; OTTAVA9; OTTA
                                                                                                                                                                                                                                                                       Name=Mrgpra; Synonyms=Mrga;
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GFCKRHODOPSN.
PROSITE; PS00237; G PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
  FUNCTION: Orphan receptor. May regulate nociceptor development, including the sensation or modulation SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S.-K., Dong X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSDFITIAWLYFLCVVLCGSSLYLLVRILCGSRKWAPLTRLYVTILLTYLVELLCGLPFGI
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Pred. No. 1.8e-50;
                                                                                                                                                                                                                                                                    Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                receptor
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tor member
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                                                                                                                                                                                                                                                                         Vertebrata;
thi; Muridae;
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; Murinae; Rattus.
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n signalin.
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                            function of pain.
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RESULT 14
Q91YB7
ID Q91YB
AC Q91YB
DT 01-DE
DT 01-DE
DT 01-MA
DE G-pro
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Matches 176
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G-protein cou
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Pfam; PF00001; 7tm 1; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane.

G-protein coupled receptor; Transmembrane.
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                              receptor
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53.3%; Pred. No. 2.1e-49;
tive 34; Mismatches 84
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Best Local
                                                               SEQUENCE FROM N.1
STRAIN=C57BL/6J;
                                                                                                                                    full insert sequence. Name=4833406I20Rik;
                                                           NCBI_TaxID=10090;
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N.A.
6J; TISSUE=Head;
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OBCDY4
OBCDY4;
O1-MAR-2003 (TrEMBLrel. 2:
     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate head cDNA, RIKEN full-length
library, clone:4833406120 product:MrgB2 G protein-couple
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
GO; GO:0007186; GPCR_Rhodopsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN_RECEP_F1_1; UNKNOWN_1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Pred. No. 4.5e-49;
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Sciurognathi; Muridae; Murinae; Rattus.
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protein-coupled recepto
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Kurihara K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Sibunitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO29369; BAC26422.1; -.
DR EMBL; AKO29369; BAC26422.1; -.
DR GO; GO:0001802; F:receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:000186; F:G-protein coupled receptor protein signalin. ..; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.
DR Fam: PF00001; 7tm 1: 1.
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STRAIN=C57BL/6J; TISSUE=Head;
STRAIN=C499374; PubMed=11042159;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=2053091; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Tashiro H., Itoh M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunuto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (Kira A., Hayashizaki Y.; tequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUB=Head;
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STRAIN=C57BL/6J; TISSUE=Head;
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STRAIN=C57BL/6J; TISSUE=Head
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851;
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PRINTS; PR00237; GPCRRHODOPSN.
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Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                               PROSITE; PS00237; PROSITE; PS50262;
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                                                        G_PROTEIN_RECEP_F1_1;
G_PROTEIN_RECEP_F1_2;
38866 MW;
7809FF78F7CEFCD6 CRC64;
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Query Match Best Local Similarity

43.3**%**; 50.0**%**;

Score 763; DB 2; Pred. No. 5.8e-48;

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ALIGNMENTS

Human; G-protein coupled; receptor; GPCR; human protease; human therapeutic protein; query sequence; search; chromosome sequence database; non-human transgenic animal; gene therapy. Human G-protein coupled receptor (GPCR). AAU97598 standard; protein; /label= Helix_1 75. .95 Location/Qualifiers label= Helix_2 337 ₿

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Matches 337; Conser
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31-MAY-2001; 2001US-00867570.
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Best Local Similarity
Matches 322; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human-derived G protein-coupled protein designated hHI77213, which is isolated from the human hippocampus. The G protein-coupled receptor can be used for preventing, treating and diagnosing genetic diseases associated with G protein-coupled protein, and for regulating cellular functions. The protein can be used to prevent and treat disorders associated with G protein-coupled protein gene dysfunction. It can also be used to identify G protein-coupled protein ligands and generating antibodies and antisers against the protein. It is also useful in constructing recombinant receptor protein expression systems, developing receptor-binding assay systems and screening drug candidates, and can be used as a probe in the genetic diagnosis of G protein-coupled protein diagnosis of G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; G protein-coupled receptor; hippocampus; diagnosis; genetic disease; cellular function regulation.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dysfunction of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human-derived G protein-coupled e.g. in determining ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G protein-coupled receptor hHI7T213 SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled protein disorders
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                                                                                                                                                                                                                                                                    MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                          RIHLDWKVLFCHVHLVSIFLSALNSSANFIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE 315
                                                                                                                                                                                                                                                     MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
                                                                                          IAMLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
                                                                                                                         CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                                                                                                                                                                      VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                              IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                95.5%;
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                                                                                                                                                                                                                                                                                                                                  Score 322; DB 3; L
Pred. No. 2.9e-309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein and encoding nucleic acid, useful treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                               Length 322;
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Best Local Similarity
Matches 322; Conserv
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12-DBC-2000;
20-FBB-2001;
20-FBB-2001;
06-APR-2001;
06-APR-2001;
06-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of several human G-protein coupled receptors (GPCRs). These can be used in the identification of candidate compounds as receptor agonists or inversagonists having applicability as therapeutic agents. The present sequent is a GPCR protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel endogenous and non-endogenous versions of G protein-coupled receptor useful for identification of candidate compounds as receptors or antagonists for use as therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; G-protein hRUP32; hRUP33; h
                                                                                                                                                                                                                                                                                                                                                      Sequence 322
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DB; ABT04875.
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                                                                                                   VSIYILNLVAADFLFLSGHIICSFLRLINIRHFISKILSFVMTFFYFIGLSMLSAISTER
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2001US-0270286P.
2001US-0282033F.
2001US-02823356P.
2001US-0282356P.
2001US-0282358P.
2001US-0292317P.
2001US-0309208P.
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2000US-0255366P.
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Matches 322
                                                                                                              The invention relates to Mrg (mas-related gene) protein, which is a G-protein coupled receptor and drg-12 protein, which is a receptor. The invention is useful for identifying compounds that bind to it, especially agonists or antagonists. Administration of an agent (e.g. the identified agonist) that increases the expression of Mrg in a mammal may be used for treating impaired sensory perception in a mammal, especially pain. The antagonist may also be useful for treating impaired sensory perception in a mammal. The present sequence is human MrgX3 protein
                                                                                                                                                                                                                                           Isolated polypeptide, Mrg, which is a G-protein coupled receptor a isolated polypeptide, drg-12, which is also a receptor, useful for identifying agonists or antagonists for treating pain.
                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2000; 2000US-0202027P.
01-AUG-2000; 2000US-0222344P.
03-NOV-2000; 2000US-00704707.
19-APR-2001; 2001US-0285493P.
                                                                                           Sequence 322 AA;
                                                                                                                                                                                                                       Claim 16; Page 130; 185pp; English.
                                                                                                                                                                                                                                                                                                                               Anderson DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAY-2001; 2001WO-US014519
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)B; AAD33751.
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mas-related gene;
                                                         Similarity
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ilarity 100.0%;
Conservative
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                                            Score 322; DB 5; Li
Pred. No. 2.9e-309;
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02-PEB-2001
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15-MAR-2001
16-MAR-2001
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2001US-0276769P

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11-APR-2001
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29-MAY-2001
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119-UN-2001
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2001US-0282992P.
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2001US-031874P.
2001US-031874P.
2001US-031874P.
2001US-031874P.
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(CURA-) CURAGEN CORP

Tchernev VT. Spytek KA, Zerhusen BD, Patturajan M, Li L, Gangolli EA, Padigaru M, Anderson DW, Raste Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wole: Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rie: ujan M, Shimkets RA;
 Rastelli L, Miller CE;
 Wolenc AR, Pena CEA;
d, Rieger DK, Burgess Cl CE CE

WPI; 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing pharmacogenomics. õ

Disclosure; SEQ ID NO 529; 1498pp; English

This invention relates to a novel nucleic acids, and encoded polypeptides CC thereof, which have properties related to the stimulation of biochemical CC or physiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for CC diagnostic and prognostic assays and furthermore in the treatment of CC diverse pathological conditions. The present invention describes novel human and murine NOVX proteins, as well as methods to modulate their CC expression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polymucleotides and antibodies are useful in CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, cc atherosclerosis, cancer and diabetes. Furthermore, they may be used in CC treating or preventing diseases such as inflammation, autoimmune CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy CC and epilepsy. Accordingly, these molecules have many activities including CC cytostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, neuroprotective, nootropic, antibacterial, virucide, antiparasitic, CC relaxant and anticonvulsant. In addition, they are useful in screening CC assays to identify small molecules that modulate or inhibit, for example, cof the propertion. This polypeptide is a homologue of a human NOVX protein of the invention. pharmacogenomics. of the invention.

Sequence

95.5%; Score 322; 몂 5 Length 322

Best Local Similarity

2.9e-309;

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31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
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31-JAN-2001;
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07-FEB-2001;
09-FEB-2001;
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27-FEB-2001;
27-FEB-2001;
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14-MAR-2001;
14-MAR-2001;
14-MAR-2001;
14-MAR-2001;
14-MAR-2001;
14-MAR-2001;
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18-JUN-2001; 2001US-02112889P.
16-AUG-2001; 2001US-03112908P.
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31-AUG-2001; 2001US-03115470P.
31-AUG-2001; 2001US-03118116P.
07-SEP-2001; 2001US-031390P.
18-OCT-2001; 2001US-03330308B.
18-OCT-2001; 2001US-03330308P.
18-OCT-2001; 2001US-03330308P.
18-OCT-2001; 2001US-03330308P.
18-OCT-2001; 2001US-03330308P.
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Gerlach Tchernev VT, nev VT. Spytek KA, Zerhusen BD, Patturaj Gangglii EA, Padigaru M, Anderson DW, Ih VI., Taupier RJ, Gusev VY, Colman SD, K., Grosse WM, Alsobrook JP, Lepley DM, Patturajan M, Shimkets son DW, Rastelli L, Mil lman SD, Wolenc AR, Pen epley DM, Rieger DK, Bu Miller CE; Pena CEA; Burgess CE;

WPI; 2002-706998/76.

New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing pharmacogenomics. õ

Disclosure; SEQ ID NO 534; 1498pp; English.

This invention relates to a novel nucleic acids, and encoded polypeptides cor thereof, which have properties related to the stimulation of biochemical cor physiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for cd diagnostic and prognostic assays and furthermore in the treatment of cc diverse pathological conditions. The present invention describes novel thuman and murine NOVX proteins, as well as methods to modulate their cexpression using antisense oligos, ribozymes and peptide nucleic acids. CC The NOVX polypeptides, polymucleotides and antibodies are useful in ctreating or preventing NOVX-associated disorders, e.g. cardiomyopathy, cc atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune cc disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig) A nephropathy, cirrhosis, cardiant, antiinflammatory, immunosuppressive, antialergic, antiastatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, celaxant and anticonvulsant. In addition, they are useful in screening creamants to identify small molecules that modulate or inhibit, for example, consured as wound healing and anoiconensis. The nucleic acids are also screening for example, ids are also

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     WPI; 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polypeptide is a homologue of a human NOVX protein of the invention.
                                                                                                                                                                                                                                                                                               psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trau
                                                  Burmer GC,
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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or diseases.

Disclosure; Fig 1; 523pp; English

CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular G CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an CC antibody against a particular GPCR, and in the production of specific CC antibody against a particular GPCR, and in the production of specific CC antibodies. The peptides and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CC CPCRs and antibodies are useful for disposing and designing drugs for treating immune-related diseases, growth-related diseases, cell CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, CC atheroselerosis, bacterial, fungal, protozoan or viral infections, CC disease Davidiscs, Crohn's disease, diabetes, graft versus host considered by the consideration of the consideration disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR protesins given in ABB81675 to ABB93018, which are used in the exemplification of the present invention

Query Match Best Local Sim. Matches 322; Sequence 322 AA; h 95.5%; Somilarity 100.0%; I 22; Conservative 0; Score 322; DB 6; Lo Pred. No. 2.9e-309; Mismatches 0 Length 322; Indels <u>,</u> Gaps

맑 S 밁 S 밁 8 S 밁 밁 S 241 181 196 121 136 61 76 16 \vdash VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER VDEGGGWLPQETLELSGSRLEQ RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPB IAMLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQMALFS IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT CLSILMPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA VDEGGGWLPQETLELSGSRLEQ RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA 322 300 315 240 180 195 120 60

ADH08535 standard; protein;

ADH08535;

25-MAR-2004 (first entry)

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Matches 322
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sensory perception;
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DB; ADH08534.
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VDEGGGWLPQBTLBLSGSRLEQ
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                                                         RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
                                                                              RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPB
                                                                                                                 IAMLVFLCVVLCGSSLVLLVRILCGSRKMFLTRLYVTILLTVLVFLLCGLFFGIQWALFS
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glaucoma; Mrg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HI7T213 protein, encoded DNA and transgenic animals for clarifying pathological mechanism, developing therapeutic methods and screening preventives or remedies for related diseases e.g. cataract, cancer, a preventives or remedies for related diseases e.g.
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                                                                                                                                                                                         CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
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                                                                              IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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Pred. No. 2.9e-309;
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RESULT 10
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           mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; colon disorder; intestinal disorder; cardiovascular disorder; muscular disorder; blood disorder; immune disorder; desorder; joint disorder; metabolic disorder; immune disorder; cancer; kidney disorder; uterus disorder; lung disorder; breast disorder; kidney disorder; uterus disorder; prostate disorder; testis disorder; skin disorder; stomach disorder; pancreas disorder; spleen disorder; thymus disorder; thyroid disorder; antiparkinsonian; antimanic; cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic; virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic; dermatological; antiulcer; antibacterial; antianaemic; anotetic;
                                                                                                                                                                                                                                                                                                                                     The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention, methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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Madisen L, Mcilwain
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09-APR-2003; 2003US-0461329P.
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lwain KL, Pavlova MN, Vassilatis D,
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CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC ansemia or leukaemda); muscular disorders; blood disorders (e.g.,
CC ansemia or leukaemda); immune disorders; blood disorders (e.g.,
CC aths); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC frautro int/mah/smiliched are commonce.
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Best Local Sim
Matches 322;
22-FEB-2002;
23-JUL-2002;
11-OCT-2002;
                                                                                                                                                                                                                   ligand; orphan receptor protein; fusion protein; fluorescent protein; cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFPuv; Enhanced GFP; EGFP; human.
                                                                                                                                                                                                                                                                                           Orphan receptor ligand-related human protein SeqID104.
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                                                                       21-FEB-2003;
                                                                                                                                             WO2003071272-A1
                                                                                                                                                                                 Homo sapiens
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2002JP-00045728.
2002JP-00213949.
2002JP-00298237.
                                                                       2003WO-JP001901
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100.0%;
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RESULT 12
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XX ADF29
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XX ADF29
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XX Human
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Best Local Similarity 100.
Matches 322; Conservative
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                                                        human; R-14; GPCR; G protein coupled receptor;
trabecular meshwork tissue; occular outflow; antagonist;
occular hypotensive; drug screening; elevated intraocular pressure;
glaucoma; ophthalmological; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transformation of cells with a fusion protein protein with a fluorescent protein useful for to the orphan receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 104; 594pp; Japanese.
                                                                                                                                               Human GPCR R-14.
                                                                                                                                                                                                             ADF29105;
                                                                                                                                                                                                                                             ADF29105 standard;
   WO2003080659-A1
                               Homo sapiens
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Pred. No.
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RESULT 13
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Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encompasses vectors and host cells comparising R-14 nucleic acids, and methods of screening for R-14 antagonists. The R-14 receptor is expressed in trabecular meshwork tissue, and is associated with a role in ocular outflow. Inhibition of the receptor results in a reduction of basal intracocular pressure, making the R-14 receptor a useful target for screening for ocular hypotensive drugs. The R-14 peptide antagonists are useful for reducing intraocular pressure for the treatment of conditions associated with elevated intraocular pressure such as glaucoma and related conditions. The R-14 receptor, and host cells expressing an R-14 polynucleotide, may be used in screening for R-14 receptor antagonists. The present sequence is related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a human GPCR (G protein coupled receptor) designated R-14 (ADF29105), nucleic acids encoding it (ADF29104), 14 peptide antagonists (ADF29106-ADF29108). The invention also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 designated R-14 (ADF29105), nucleic acids er 14 peptide antagonists (ADF29106-ADF29108).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           YFIGLSMLSAISTERCLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLF
                                                                                                                                                                                                                                                  NLKLVLQRALQDTPEVDEGGGWLPQETLELSGSRLEQ 337
                                                                                                                                                                                                                                                                                                                     LLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQ
                                                                                                                                                                                                                                                                                                                                                                                        SGADSVWCETSDFITIAWLVFLCVVLCGSSLVLLVRILCGSRKMFLTRLYVTILLTVLVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.2%; Score 277; DB 8; Lilarity 100.0%; Pred. No. 8.6e-265; Conservative 0; Mismatches
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Human; novel G-protein coupled receptor; signal transduction;

Human novel G-protein coupled receptor #1

19-DEC-2000

(first entry)

AAB14846 standard;

protein;

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RESULT 14
AAY90762
ID AAY90
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AC AAY90
AC AAY90
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the protein sequence for a novel human G-protein coupled receptor (NGPCR). These proteins are involved in signal transduction pathways in many cases. The protein contains seven transmembrane domains, and is expressed in human testis, mammary gland and salivary gland tissue. The protein, its gene, agonists, antagonists and antibodies can be used to diagnose and treat diseases associated with the inappropriate expression or expression of mutant versions of the protein, for screening for drugs which can be used in the same manner, and for elucidating the function of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding novel G-protein coupled diagnosis, drug screening, clinical trial monitoring treatment of physiological or behavioral disorders.
                            Human; G protein-coupled receptor; hippocampus; genetic disease; cellular function regulation.
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N-PSDB; AAA70342.
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14-JAN-1999;
                                                            Human G protein-coupled receptor hHI7T213V SEQ ID NO:2.
                                                                                    18-AUG-2000
                                                                                                                             AAY90762 standard; protein; 322
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 322
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Local Similarity 100.0%; F
1es 224; Conservative 0;
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99US-0115828P.
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                                                                                                                                                                                                                                                                                                                                                             Score 224; DB 3; Lo
Pred. No. 2.1e-212;
0; Mismatches 0;
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                                       diagnosis;
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                                        screening
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                              ADI16994;
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                                                  standard; protein; 322
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
          (first
          entry)
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The present sequence represents a human-derived G protein-coupled protein designated hHI7T213V, which is isolated from the human hippocampus. The G protein-coupled receptor can be used for preventing, treating and diagnosing genetic diseases associated with G protein-coupled protein, and for regulating cellular functions. The protein can be used to prevent and treat disorders associated with G protein-coupled protein gene dysfunction. It can also be used to identify G protein-coupled protein ligands and generating antibodies and antisera against the protein. It is also useful in constructing recombinant receptor protein expression systems, developing receptor-binding asset yestems and screening drug candidates, and can be used as a probe in the genetic diagnosis of G protein-coupled protein disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 92-93; 97pp; Japanese.
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                                    VDEGGGWLPQETLELSGSRLEQ
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VDEGGGWLPQETLELSGSRLEQ
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                                                                                                                                                                                                                                                                                       IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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Pred. No. 1.9e-209;
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08 - FEB - 2001
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115 - FEB - 2001
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2001US-0265514P.
2001US-0266406P.
2001US-0266976P.
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Tchernev VT, Spytek KA, Zerhusen BD Li L, Gangolli EA, Padigaru M, And Gerlach VL, Taupier RJ, Gusev VY, Furtak K, Grosse WM, Alsobrook JP, Anderson DW, R VY, Colman SD, JP, Lepley DM, BD, Patturajan M, Rastelli L, Wolenc AR, Molenc DK, Shimkets RA; li L, Miller CB; Pena CEA; Burgess CE;

2002-706998/76

pharmacogenomics. atherosclerosis, treating polypeptides and nucleic acids, useful involvation of the normal series of the polypeptides and inchromosome the normal series or diabetes, and in chromosome the normal series of the normal series o ids, useful for preventing ce.g. cancer, cardiomyopathy, chromosome mapping, tissue typing 8

Disclosure; SEQ ID NO 530; 1498pp; English

This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical corphysiological responses in a cell, tissue, organ or organism. CC Specifically, it refers to the use of biologically active fragments for cd diagnostic and prognostic assays and furthermore in the treatment of cd diagnostic and prognostic assays and furthermore in the treatment of cd diagnostic and prognostic assays and furthermore in the treatment of cd thuman and murine NOVX protectins, as well as methods to modulate their carpression using antisense oligos, ribozymes and peptide nucleic acids. The NOVX polypeptides, polymucleotides and antibodies are useful in ctreating or preventing NOVX-associated disorders, e.g. cardiomyopathy, cd atherosclerosis, cancer and diabetes. Furthermore, they may be used in ctreating or preventing diseases such as inflammation, autoimmune cd disorders, allergies, blood disorders, acquired immunodeficiency syndrome contributes. Alzheimer's disease, infections, stroke, muscular dystrophy carthritis, Alzheimer's disease, infections, stroke, muscular dystrophy carthritis, Alzheimer's disease, infections, stroke, muscular dystrophy contributed application, antiinflammatory, immunosuppressive, antialergic, antiasteriosclerotic, anorectic, antiastatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic, consense to identify small molecules that medulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and of the invention. pharmacogenomics. of the invention.

Sequence 322 A,

Query Match

Local

Similarity

65.6%;

DB 5; 1

Length 322;

δ δ δ 문 δ 문 밁 ঠ 문 片 S Matches 316 241 196 301 256 181 121 136 321; 19 76 16 IAMLVELCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVELLCGLPFGIQWALFS CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT MDSTIPVLGTBLTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA VDEGGGWLPQETLELSGSRLEQ RIHLDWKVLFCHVHLVSIFLSALNSSANFIIYFFVGSFRQRQNRQNLKLVLQRALQDTFE CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMPCDPLFSGANSVWCETSDFIT MDSTIPVLGTELTPINGREETPCYKQTLSPTGLTCIVSLVALTGNAVVLWLLGCRWRRNA VDEGGGWLPQETLELSGSRLEQ RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE Conservative 0 Score 221; DB Pred. No. 1.9e 0; Mismatches 337 Indels 0 Gaps 300 255 180 120 135 60 240 75 0

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Search completed: October 27, 2004, 08:48:14 Job time: 156 secs

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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 60.0 , Gapext 60.0
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US-09-255-368-8
US-09-405-588-8
US-09-405-588-15
US-09-104-360A-15
US-09-104-360A-15
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US-09-254-227A-5
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APPLICANT: Ahmad, St
APPLICANT: Banville,
APPLICANT: Fortin, V
APPLICANT: Lembo, Pe
                                                                                       Sequence 5, Application US/09254227A Patent No. 6696257
    APPLICANT:
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Ahmad, Sultan Banville, Denis Fortin, Yves Lembo, Paola O'Donnell, Dajan

JS-09-254-227A.3 Sequence 3, Application US/09254227A Patent No. 6696257 GENERAL INFORMATION: APPLICANT: Almad, Sultan APPLICANT: Manual, Sultan APPLICANT: Fortin, Yves APPLICANT: Fortin, Yves APPLICANT: Coronnell, Dajan APPLICANT: Coronnell, Dajan APPLICANT: O'Donnell, Dajan APPLICANT: Shi-Hsiang, Shen TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human FILE REFERENCE: 81823/268117 CURRENT APPLICATION NUMBER: US/09/254,227A CURRENT APPLICATION NUMBER: US/09/254,227A CURRENT APPLICATION NUMBER: US/09/254,227A CURRENT APPLICATION NUMBER: US/09/254,227A CURRENT APPLICATION NUMBER: 1999-03-03 NUMBER OF SEQ ID NOS: 22 SOCFTWARE: Patentin version 3.0 SEQ ID NO 3 LENGTH: 322 TYPE: PRT ORGANISM: Homo sapiens JEON-254-227A-3 GUOTY Match Best Local Similarity 100.0%; Pred. No. 4.4e-134; Best Local Similarity 200.0%; Pred. No. 4.4e-134; Best Local Si	ALIGNMENTS .	28 7 2.1 65 1 US-08-055-917-16 Sequence 16, Appl 30 7 2.1 65 1 US-08-095-068-14 Sequence 14, Appl 31 7 2.1 65 1 US-08-095-068-16 Sequence 14, Appl 31 7 2.1 65 1 US-08-140-721A-16 Sequence 16, Appl 32 7 2.1 65 1 US-08-140-721A-16 Sequence 16, Appl 32 7 2.1 65 1 US-08-140-721A-16 Sequence 16, Appl 33 7 2.1 65 1 US-08-619-790C-14 Sequence 16, Appl 35 7 2.1 65 1 US-08-619-790C-16 Sequence 16, Appl 35 7 2.1 65 2 US-07-785-563A-16 Sequence 16, Appl 36 7 2.1 71 1 US-08-055-917-17 Sequence 17, Appl 38 7 2.1 71 1 US-08-055-917-17 Sequence 17, Appl 40 7 2.1 71 US-08-095-068-15 Sequence 17, Appl 41 7 2.1 71 US-08-095-068-15 Sequence 17, Appl 42 7 2.1 71 US-08-095-068-15 Sequence 17, Appl 43 7 2.1 71 US-08-140-721A-17 Sequence 17, Appl 44 7 2.1 71 US-08-140-721A-17 Sequence 17, Appl 44 7 2.1 71 US-08-140-721A-17 Sequence 17, Appl 44 7 2.1 71 US-08-15-565A-15 Sequence 17, Appl 45 7 2.1 71 US-08-619-790C-15 Sequence 17, Appl 45 7 2.1 71 US-08-619-790C-15 Sequence 17, Appl 45 7 2.1 71 US-08-619-790C-15 Sequence 17, Appl 45 7 2.1 71 US-08-15-565A-15 Sequence 17, Appl 55 7 2.1 71 US-08-15-565A-15 Sequence 17, Appl 55 7 2.1 71 US-08-15-565A-15 Sequence 17, Appl 55 7 2.1 71 US-08-15-565A-15 Sequence 18, Appl 55 7 2.1 71 US-08-15-565A-15 Sequence	
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PATENT APPLICANT NO. 6696257

GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Fortin, Yves
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Haiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
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GENERAL INFORMATION:
                                                                                                                                                                                                                                            Sequence 7, Application US/09254227A Patent No. 6696257
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LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Lembo, Paola
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
COUNTAINE: Details 1299-03-03
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APPLICANT:
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APPLICANT:
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CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    248 VLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQD 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                             14.8%; Score 50; DB 4;
100.0%; Pred. No. 1.6e-3
tive 0; Mismatches
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US-09-254-227A-13
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Best Local Similarity
Matches 44; Conserv
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LENGTH: 322
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
                                                            SEQ ID NO 13
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Best Local (
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                                                                                                                                                                                                                                                                                                 Patent No. 66962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
                                                                                                                              APPLICANT: Shi-Heiang, Shen
APPLICANT: Shi-Heiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat
PTILE REFERENCE: 81823/268117
PTILE REFERENCE: 81823/268117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
                                                                                                              CURRENT APPLICATION NUMBER: US/09/254,227A CURRENT FILING DATE: 1999-03-03
                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                APPLICANT:
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                                                                               SOFTWARE:
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ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
             TYPE: PRT
ORGANISM: Homo
                                              LENGTH: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     209 SSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGI 249
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                                                                                                                                                                                                                                                                                                                13, Application US/09254227A
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Fortin, Yves
Lembo, Paola
Lombo, Paola
O'Donnell, Dajan
O'Luaiang, Shen
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Banville, uc...
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Lembo, Paola
O'Donnell, Dajan
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Fortin, Yves
                                                                                 PatentIn version 3.0
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Query Match

12.2%;

Score 41;

DB 4;

Length 322;

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; SOFTWARE: Pat.
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRT
; ORGANISM: rat
US-09-254-227A-1
RESULT 9
US-09-255-368-8
; Sequence 8, Application US/09255368
; Patent No. 6262246
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Best Local Similarity
Matches 11; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: GARY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10936, Application US/09489039A Patent No. 6610836
                                                                                                                                                               Matches
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Best Local Similarity
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SEQ ID NO 10936
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Shi-Heiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 2709.2004001
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                                                                                                                                                                                                                                       ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                          LENGTH: 773
                                                                                                                             271 VSIFLSALNS 280
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Lembo, Paola
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Banville, Denis
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Pred. No. 0.029;
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                                                                                                                                                                            DB 4;
0.56;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-255-368-8
                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-405-558-8
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US-09-405-558-8
                                                                                                      US-08-978-404B-31
                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/0940558A
Patent No. 6709831
GENERAL INFORMATION:
APPLICANT: Gertald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
APPLICANT: Borowsky, Beth E.
APPLICANT: Borowsky, Beth E.
APPLICANT: Craig, Douglas A.
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF
FILE REFERENCE: 57155-C.
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver.
SEQ ID NO 8
LENGTH: 430
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                                                                 Sequence 31, Application US/08978404B Patent No. 5968782
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/405,558A CURRENT FILING DATE: 1999-09-24 EARLIER APPLICATION NUMBER: 09/161,113 EARLIER FILING DATE: 1998-09-25 EARLIER APPLICATION NUMBER: 09/255,368 EARLIER FILING DATE: 1999-02-22 NUMBER OF SEQ ID NOS: 71
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CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 09/161,113
EARLIER FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 42
GENERAL INFORMATION:
APPLICANT: Stevens,
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT: Jones, Kenneth A.
APPLICANT: Bonini, James A.
APPLICANT: Bonini, James A.
APPLICANT: Borowsky, Beth
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: 1795/57155-A
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                  Richard L.
MAST CELL PROTEASE THAT CLEAVES
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Pred. No.
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NUMBER OF SEQUENCES:

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RESULT 12
US-09-016-366A-15
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Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
                                                                                                                      COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPB: Diskett
                                                                                                                                                                                                                                                 APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637 REFERENCE/DOCKET NUMBER: BOITELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1i
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ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEB: Wolf, Gre
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TOPOLOGY: linear
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                                                                                                                          Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8;
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US-08-978-404B-21
                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer; Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
REFERENCE/DOCKET NUMBER: B0801/7090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Steven
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                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 276 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
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LENGTH: 276 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                  MOLECULE TYPE: No. 5968782e
                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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Local Similarity 100.0%; Pred. No. 18;
les 8; Conservative 0; Mismatches
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REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
                                    STRANDEDNESS:
TOPOLOGY: lir
                                                                        TYPE: amino acids
                                                                                                                                                                       TELEFAX:
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MAST CELL PROTEASE THAT CLEAVES
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APPLICANT: Gerald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
APPLICANT: Bonini, James A.
APPLICANT: Bonini, James A.
APPLICANT: Borowsky, Beth
TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
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US-09-255-368-2
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US-09-134-001C-3801
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Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEPLEMMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR TILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3801
LENGTH: 428
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Patent No. 6262246
GENERAL INFORMATION:
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                                                                                                                                                Query Match 2.4%; Score 8; DB: Best Local Similarity 100.0%; Pred. No. 27 Matches 8; Conservative 0; Mismatches
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324 SSANPITY 331
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100.0%; Pred. No. 18;
active 0; Mismatches
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No. 27;
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Search completed: October 27, 2004, 08:52:22 Job time : 42 secs

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Maximum
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                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seg length: 2000000000
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Gapop 60.0 , Gapext 60.0
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337
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                                                                                                                                                                       /Ggn2_6/ptodatta/1/pubpaa/USO7_NEW_PUB.pep:*
/Ggn2_6/ptodatta/1/pubpaa/PCTUS_PUBCOMB.pep:*
/Ggn2_6/ptodatta/1/pubpaa/USO8_REW_PUB.pep:*
/Ggn2_6/ptodatta/1/pubpaa/USO8_PUBCOMB.pep:*
/Ggn2_6/ptodatta/1/pubpaa/USO8_PUBCOMB.pep:*
/Ggn2_6/ptodatta/1/pubpaa/USO9E_PUBCOMB.pep:*
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SUMMARIES
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US-10-292-798-1274 US-10-072-012-530 US-10-072-012-535	US-10-072-012-534 US-10-219-834-79 US-10-401-397A-2 US-10-391-074-2	US-09-995-225-20 US-09-995-225-20 US-10-183-116-31 US-10-225-567A-674 US-10-072-012-529	ID US-09-867-570-2
	Sequence 534, App Sequence 79, Appl Sequence 2, Appli Sequence 2, Appli	27101	Description Sequence 2, Appli

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ALIGNMENTS

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NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 337
TYPE: PRT
ORGANISM: Human
US-09-867-570-2
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Publication No. US20040076951A1

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL009900-CIP
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 337; Conserv
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CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/695,045
PRIOR FILING DATE: 2000-10-25
121 YPIGLSMLSAISTERCLSILWPIWYHCRRPRYLSSVMCYLLWALSLLRSILEWMFCDFLF 180
                                                                                                 61 AVVLWLLGCRMRRNAVSIYILNLVAADFLFLSGHIICSFLRLINIRHPISKILSFVMTFF 120
                                                                    61 AVVLWLIGCRMRRNAVSIYILNIVAADFIFISGHIICSFIRLINIRHFISKILSFVMTFP
                                                                                                                                                                                        1 MESKSSWVIRLGFLSMDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGN
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                                                                                                                                                                                                                                                    100.0%; Score 337; DB 11; ilarity 100.0%; Pred. No. 4.1e-300; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 322; Conserv
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PRIOR FILING DATE: 2001-07-31
NUMBER OF COLUMN NUMBER 
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APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 67 SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
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PRIOR APPLICATION NUMBER: 60/282,032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,366
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/270,286
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
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CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
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APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0308
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 322
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FILING DATE: 2001-04-06
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VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
                                                                                       MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
                                                                                                                                                                                                                                                      95.5%; Score 322; DB 9; Li
ilarity 100.0%; Pred. No. 2.2e-286;
Conservative 0; Mismatches 0;
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; OTHER INFORMATION: NO. US-09-995-225-20
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CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR PILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 1998-10-13
PRIOR PILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 322
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Publication No.
Best Local Similarity Matches 322; Conserv
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                                             Query Match
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APPLICANT: Chu, Zhi Liang
APPLICANT: Chu, Zhi Liang
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/282,365
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-07
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/282,356
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/282,358
PRIOR FILING DATE: 2001-04-06
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PRIOR FILING DATE: 2001-02-20
                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                TYPE: PRT
                                                                                                                                    FEATURE:
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No. US20030139588A9
    Conservative
95.5%; Score 322; DB 10;
100.0%; Pred. No. 2.2e-28;
ive 0; Mismatches 0
                                                                                                             US20030139588A9el Sequence
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TITIE OF INVENTION: BAIN SIGNALING MOLECULES
FILLE REFERENCE: CALTE.4C1CP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 69/704,707
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR APPLICATION NUMBER: US 09/85,493
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 109
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US-10-183-116-31
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Best Local Similarity
Matches 322; Conserv
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SEQ ID NO 31
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APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
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                   CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT
                                  CLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFIT 195
                                                                                                        VSIYILNLVAADFLFLSGHIICSFLRLINIRHPISKILSFVMTFFYFIGLSMLSAISTER
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100.0%; Pred. No. 2.2e-286;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 674
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
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; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Boumer, Glenna C.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: BURMER; GLENIC PEPTIDES AN
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AN
; FILE REFERENCE: 1920-4-4
                                                                                                    RESULT 6
US-10-072-012-529
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                                                    Sequence 529, Application US/10072012 Publication No. US20040033493A1 GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 322;
APPLICANT: Tchernev, Velizar APPLICANT: Spytek, Kimberly APPLICANT: Zerhusen, Bryan
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APPLICANT: BUTGESS, Catherine B.
APPLICANT: BUTGESS, Catherine B.
FILE REFERENCE: 21402-258
CURRENT APPLICATION PROTEINS and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/255,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR PILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,406
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR TILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
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US-10-072-012-529
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PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
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VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER
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Grosse, William M.
Alsobrook II, John P.
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Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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Rieger, Daniel K.
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Wolenc, Adam
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Shimkets, Richard
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CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
Query Match
Best Local Similarity
Matches 322; Conser
                                                                                                                                        SEQ ID NO 534
LENGTH: 322
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APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
FILE REFERENCE: 21402-258
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                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
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PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
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PRIOR FILING DATE: 2001-02-02
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PRIOR FILING DATE: 2001-02-05
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: Spytek, Kimberly
: Zerhusen, Bryan
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Anderson, David W.
Rastelli, Luca
Miller, Charles E.
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Grosse, William M.
Alsobrook II, John P.
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Taupier Jr, Raymond J.
Gusev, Vladimir Y.
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o. US20040033493A1
95.5%; Score 322; DB 15; ilarity 100.0%; Pred. No. 2.2e-286; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2001-08-20
PRIOR PPLICATION NUMBER: US 60/340,703
PRIOR PPLICATION NUMBER: US 60/340,703
PRIOR PPLICATION NUMBER: US 60/318,675
PRIOR APPLICATION NUMBER: US 60/318,675
PRIOR PPLICATION NUMBER: US 60/355,596
PRIOR PILING DATE: 2001-09-12
PRIOR PILING DATE: 2002-02-06
PRIOR PPLICATION NUMBER: US 60/333,417
PRIOR PILING DATE: 2001-11-66
PRIOR PPLICATION NUMBER: US 60/338,367
PRIOR PILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 192
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Best Local Similarity
Matches 287; Conserv
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TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF
FILE REFERENCE: D0191 NP
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CURRENT FILING DATE: 2002-08-15
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                                Sequence 2, Application US/10391074

Publication No. US20040038345A1

GENERAL INFORMATION:

APPLICANT: Wehls, Michael

APPLICANT: Wattler, Frank

TITLE OF INVENTION: No. US20040038345A1el Hur

FILE REFERENCE: 7705.0008-00-000

CURRENT APPLICATION NUMBER: US/10/391,074

CURRENT FILING DATE: 2003-03-17

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 322
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; TYPE: PRT
; ORGANISM: Homo s
US-10-401-397A-2
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US-10-391-074-2
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US-10-401-397A-2
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Best Local Similarity
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APPLICANT: Moffett, Serge
APPLICANT: Abran, Daniel
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                  Human Seven-Transmembrane Receptors
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HITLE OF INVENTION: METHODS AND COMPOUNDS FOR TITLE OF INVENTION: INTRAOCULAR PRESSURE AND FILE REFERENCE: 4518/1M674US1
CURRENT APPLICATION NUMBER: US/10/401,397A
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 60/367,513
PRIOR PILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                          121 YFIGLSMLSAISTERCLSILWPIWYHCRRPRYLSSVMCVLLWALSLLRSILEWMFCDFLF 180
                                     301 NIKIVIORALODTPEVDEGGGWIPOETLELSGSRIEQ 337
                                                                                                                                                                                                           181 SGADSVWCETSDFITIAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVF
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                                                                                                                                                                                                                                                                                                                                   NLKLVLQRALQDTPEVDEGGGWLPQETLELSGSRLEQ
                                                                                                                          LLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQ
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                                                                                                                                                                    SGADSVWCETSDFITIAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVF
                                                                                LLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQ
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100.0%; Pred. No.
1ve 0; Mismatches
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Pred. No. 3.6e-245;
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AND
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  322
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-1274
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US-10-292-798-1274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 08435/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION UNMBER: 10/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1274, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
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-- incal Similarity
Conserv
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Best Local Similarity 99.7%;
Matches 321; Conservative
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIRO
                                                                                                             181
                                                                                                                                               196
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                                                         256 RIHLDWKVLFCHVHLVSIFLSALNSSANFIIYFFVGSFRQRQNRQNLKLVLQRALQDTFE 315
                                                                                                                                                                                                     136 CLSILWPIWYHCRRPRYLSSVMCVLLWALSILRSILEWMFCDFLFSGADSVWCETSDFIT 195
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VDEGGGWLPQETLELSGSRLEQ 337
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Pred. No. 7.2e-194; 
0; Mismatches 1; Indels
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US-10-072-012-530
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CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR FILING DATE: 2001-01-31
                                                                     Query Match
Best Local Similarity
Matches 321; Conserv
                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 530
LENGTH: 322
TYPE: PRT
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Publication No. US20
GENERAL INFORMATION:
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APPLICANT: Spytek, I
APPLICANT: Zerhusen
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PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR APPLICATION NUMBER: 60/266,767
                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1391
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
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PRIOR FILING DATE: 2001-02-07
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Taupier Jr, Raymond J.
Gusev, Vladimir Y.
Colman, Steven D.
Wolenc, Adam R.
Pena, Carol B. A
                  MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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MDSTIPVLGTELTPINGREETPCYKQTLSFTGLTCIVSLVALTGNAVVLWLLGCRMRRNA
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Grosse, William M.
Alsobrook II, John P.
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Rieger, Daniel K.
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Shimkets, Richard
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Zerhusen, Bryan
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5. US20040033493A1
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                                                                                           65.6%;
                                                                                       Score 221; DB 15;
Pred. No. 7.2e-194;
                                                                         Mismatches
                                                                                                            Length 322;
                                                                         Indels
                                                                         0
                                                                         Gaps
                                      75
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ARPHICANT: ALEGEL, CALLEGIA B.
ARPHICANT: BUTGESS, CALLEGIA B.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR RILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-08
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US-10-072-012-535
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APPLICANT: Spytek, Kimberly
APPLICANT: Serhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkete, Richard
APPLICANT: Shimkete, Richard
APPLICANT: Gangolli, Bsha
APPLICANT: Padigaru, Muralidh
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Gosev, Vladimir Y.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Alsobrook II, John
APPLICANT: Alsobrook II, John
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Rastelli, Luca
Miller, Charles E.
Gerlach, Valerie
Taupier Jr, Raymond of
Gusev, Vladimir Y.
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Grosse, William M.
Alsobrook II, John P.
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Rieger, Daniel K.
Burgess, Catherine B.
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Shimkets, Richard
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p. US20040033493A1
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US-10-072-012-535
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                                                                                                                                                                   SOFTWARE: Patentin Ver. 2
SEQ ID NO 10
LENGTH: 302
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                         US-10-237-467-10
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NUMBER OF SEQ ID NOS: 1391
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 535
LENGTH: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:
                                                               Matches
                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                              TITLE OF INVENTION: Sensory Neuron Receptors FILE REFERENCE: 021288-001300US CURRENT APPLICATION NUMBER: 9203-01-14 PRIOR APPLICATION NUMBER: US 60/317,879 PRIOR FILING DATE: 2001-09-07 NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liao, Jiayu
APPLICANT: Gray, Nathanael S.
APPLICANT: Caldwell, Jeremy C.
APPLICANT: Schultz, Peter G.
APPLICANT: IRM LLC
                                                                                                                                       OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR) OTHER INFORMATION: 7 (DRG7) (NT009307)
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281;
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                                                                            Similarity
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Pred. No. 7.2e-194;
                                                                          Score 181; DB 14; Length 302; Pred. No. 3e-157;
                                                               Mismatches
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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASIJAMI, HIROYUKI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
FULE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: UP 2001/246789
PRIOR FILING DATE: 2001-6-18
NUMBER OF SEQ ID NOS: 2430
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1600
LENGTH: 197
Search completed: October 27, 2004, 09:03:34 Job time : 133 secs
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; ORGANISM: Homo sapiens
US-10-017-161-1600
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US-10-017-161-1600
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Publication No. US20030143668A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  Query Match 38.9%; Score 131; DB 14; Length 197; Best Local Similarity 100.0%; Pred. No. 1.3e-111; Matches 131; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 RONRONLKLVLQRALQDTPEVDEGGGWLPQETLELSGSRLEQ 337
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121 CLSILWPIWYH 131
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                                                                                                                                 VSIYILNLVAADFLFLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTER 135
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                                                                                         Post-processing: Listing first 45 summaries
                                                                                                                                                                Total number of hits satisfying chosen parameters:
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length: 2000000000
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337
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pir1: *
pir2: *
pir3: *
pir4: *
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(without alignments)
831.412 Million cell updates/sec
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                                                                                                                                                                                                                            96216763 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

7 2.1	7 3 1	7 2.1	7 2.1	, 2.1	3	7 2.1	7 2.1	7 2.1	7 2.1	7 2.1	7 2.1	7	7	7	8 2.4	8 2.4	.4	8 2.4	8 2.4	8 2.4	8 2.4	8 2.4	8 2.4	2.4	8 2.4	2.4	2.4	2 10 3.0 4	1 14 4.2 3	Score	Result Ouerv
213	9	99	186	101	2	79	174	163	160	125	71	71	50	49	984	541	541	455	429	411	276	230	215	215	41	141	111	435	78	•	
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nypothetical prote		puromycin N-acetyl	conserved hypothet			hypothetical prote	H de		lis YdbS	pothetical	hain	Ig alpha-1 chain C		ting	hypothetical WD-re			hypothetical prote	m	hypothetical prote	mast cell proteina	mast cell proteina						Antho-RFamide prec	transforming prote	Description	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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324	322	315	313	303	301	300	298	284	276	270	269	263	260	256	256
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TVRTAS	T24525	T49982	AB2203	B96909	F86440	T26245	F82356	AH0415	S35270	S16579	C71255	S48498	AI2481	AD1480	AI1119
transforming prote	hypothetical prote	hypothetical prote	hypothetical prote	probable permease	unknown protein [i	hypothetical prote	transcription acti	probable membrane-	DNA-damage repair	chitinase (EC 3.2.	conserved hypothet	oxidoreductase hom	hypothetical prote	transcription regu	transcription regu

ALIGNMENTS

C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: A39485
R;Monmot, C.; Weber, V.; Stinnakre, J.; Bihoreau, C.; Teutsch, B.; Corvol, P.; Clauser, I Mol. Endocrinol. 5, 1477-1487, 1931
Mol. Endocrinol. 5, 1477-1487, 1931
A;Title: Cloning and functional characterization of a novel mas-related gene, modulating A;Reference number: A39485; MUID:92130997; PMID:1723144

transforming protein (mrg) - human

A; Accession: A39485

A;Status: preliminary

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RESULT 2
AA4308
Antho-RFamide precursor - sea anemone (Anthopleura elegantissima)
C.Species: Anthopleura elegantissima
C.Species: Anthopleura elegantissima
C.Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Accession: A44308
C.Schmutzler, C.; Darmer, D.; Diekhoff, D.; Grimmelikhuijzen, C.J.
J. Biol. Chem. 267, 22534-22541, 1992
J. Biol. Chem. 267, 22534-22541, 1992
J. Hibertification of a novel type of processing sites in the precursor for the A;Reference number: A44308; MUID:93054550; PMID:1429603
                                                                                                                                                                        A;Cross-references: UNIPROT:P10419; GB:M98269; NID:g155702; PIDN:AAA27738.1; A;Note: sequence extracted from NCBI backbone (NCBIN:117102, NCBIP:117104) C;Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-378 <MON5
A; Residues: 1-378 <MON5
A; Cross-references: UNIPROT: P35410; GB: S78653; NID: g244209; PIDN: AAB21255.1; PID: g244210
C; Superfamily: mas transforming protein
C; Keywords: G. protein-coupled receptor; transmembrane protein
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A;Molecule type: mRNA; protein
A;Residues: 1-435 <SCH>
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                                                                                 Query Match 3.0%; So
Best Local Similarity 100.0%; F
Matches 10; Conservative 0;
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                                          230 YVIILLIVLV 239
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YVTILLTVLV 15
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100.0%; Pred. No. 6.2e-06;
                                                                                      Score 10; DB; pred. No. 0.0
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                                                                                                           DB 2;
0.085;
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hypothetical protein NMA1940 [imported] - Neisseria meningitidis (strain Z2491 C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C;Accession: B81822 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; RaNature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81055
R;Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viscotoxin - European mistletoe
C;Species: Viscum album (European mistletoe)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S16099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <PAI
                                                              A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-141 <TET>
A; Cross-references: UNIPROT: Q9JY98;
A; Cross-references: erogroup B,
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A; Accession: C81055
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A; Residues: 1-111 <EUR>
C; Superfamily: viscotox
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Eur. J. Biochem. 198, 549-553, 1991
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|Species: Neisseria meningitidis
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Best Local Similarity
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DNA
1 <PAR>
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llarity 100.0%; Pred. No.
Conservative 0; Mismatc
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strain MC58
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J. Mol. Endocrinol. 9, 283-289, 1992
A;Title: Cloning of a bullfrog growth hormone cDNA: exp A;Reference number: I51188; MUID:93119453; PMID:1476615 A;Reference T51188
                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <TAK>
                                                                                                                                                                                                                                                                             N;Alternate names: growth hormone
C;Species: Rana catesbeiana (bullfrog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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JS0037
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                                                                                                  A;Cross-references: UNIPROT:P10813; GB:S52027; NID:g262921; PIDN:AAB24792.1; PID:g262922 C;Superfamily: prolactin
                                                                                                                                                                                                                                                       C;Accession: I51188
R;Takahashi, N.; Kikuyama,
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C;Keywords: growth factor; hormone
F;1-25/Domain: signal sequence #status predicted <SI
F;26-215/Product: somatotropin #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 26-55 <PA2>
G;Comment: This protein is synthesized and secreted G;Superfamily: prolactin
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A; Residues: 1-215 < PAN>
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A;Title: Cloning and sequencing of bullfrog
A;Reference number: JS0037; MUID:88252154; P
A;Accession: JS0037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: JS0037; PS0310 R; Pan, F.M.; Chang, W.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rana catesbeiana (bullfrog)
C;Date: 31-Mar-1992 #sequence_revision
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A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                         somatotropin - bullfrog
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                                 Best Loc
Matches
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                                                  Local
 208 GSSLVLLV 215
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                               Similarity
8; Conserv
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                                   Conservative
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                             2.4%; Score 8; DB :
100.0%; Pred. No. 5.:
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A;Cross references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509
R;Cross references: GB:M57626; NID:g200508; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A;Title: Different mouse mast cell populations express various combinations of at least A;Reference number: A35646; MUID:90222202; PMID:2326280
A;Accession: D35646
A;Molecule type: protein
A;Residues: 32-54 <RE3>
R;Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson, Scand. J. Immunol. 38, 359-367, 1993
A;Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and A;Reference number: I59478; MUID:94023807; PMID:8210998
A;Accession: I59478
A;Accession: I59478; MUID:94023807; PMID:8210998
A;Accession: I59478; MUID:94023807; PMID:8210998
A;Accession: I59478; MUID:94023807; PMID:8210998
A;Accession: GB:G31853; NID:g473480; PIDN:AAA39725.1; PID:g473481
C;Genetics:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A38654
A;Molecule type: DNA
A;Residues: 1 276 <REY>
A;Cross-references: UNIPR
A;Note: the authors trans
s Gly, GAG for residue 14
A;Accession: B38654
A;Molecule type: mRNA
A;Residues: 1-276 <REZ>
C;Gene: WMCP-6
A;Gene: MMCP-6
A;Introns: 24/1; 79/2; 168/1; 222/3
A;Introns: 24/1; 79/2; 168/1; 222/3
A;Introns: 24/1; 79/2; 168/1; 222/3
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
C;Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-31/Domain: activation peptide #status predicted <ACT>
F;22-31/Domain: dignal cell proteinase 6 #status experimental <MAT>
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A;Title: Genes for mast-cell serine protease and their molecular evolution. A;Reference number: I48684; MUID:95048582; PMID:7959952
A;Accession: I48685
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mENA
A;Molecule type: mENA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: UNIPROT:P21845; GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g20050; Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37 (Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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8; Conservative 0;
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A; Gene:
A; Map po
                    A, Experimental source: strain 9a5c

A, Experimental source: strain 9a5c

R, Simpson, A, J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H

as-Neto, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A, Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme

J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.B.; Laigre

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.

A, Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasakı

A, Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira,

M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze

A, Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below A;Accession: F82679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein XF1453 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: F82679
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A;Cross-references: UNIPROT:074310; EMBL:AL031349; PIDN:CAA20480.1;
A;Experimental source: strain 972h-; cosmid c15D4
C;Genetics:
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A;Accession: T39481
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F;75,122,225/Active site: His, Asp, Ser #status predicted
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A; Contents: annotation
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milarity 100.0%;
Conservative 0
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Pred. No.
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-541 <KUR>
A;Cross-references: UNIPROT:Q8UBY5; GB:AE008688; PIDN:AAL43694.1; PID:g17741221; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein thiP [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AH2909
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A;Molecule type: DNA
A;Residues: 1-455 <KUN>
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Puma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero, A; Muthors: Yoshikawa, H.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, K.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                  A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550; A; Accession: AH2909
                                                                                                                                                                                                                                                                    ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li,
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C;Superfamily: Bacillus subtilis hypothetical protein yycH
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A;Experimental source: strain 168
C;Genetics:
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influenzae conserved hypothetical protein HI1590
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T50309
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97684
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A; Residues: 1-984 < BRO>
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A; Map position: ci
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A;Molecule type: DNA
A;Residues: 1-541 <KUR>
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Best Local Similarity 100.0%;
Matches 8; Conservative
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Best Local
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les 8; Conserv
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                                           280 SSANPILY 287
                                                                                                                                                                                                                                                                                                                                                                                    .; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
to the EMBL Data Library, November 1999
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kelz, B.;
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Search completed: October 27, 2004, 08:53:08 Job time : 41 secs

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Result
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Perfect score:
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L.H., Derge J.G., Shenmen C.M., Schuler G.D., Schaefer C.F., Bhat N.K., S.I., Wang J., Hsieh F., Casavant T.L., Scheetz T.E., Carninci P., Prange C., Abramson R.D., Mullahy S.J., Malek J.A., Gunaratne P.H., isa A.M., Gay L.J., Hulyk S.W., J., Lu X., Gibbs R.A., J., Lu X., Gibbs R.A., J., Lu X., Gibbs R.A., J., Bouffard G.G., Myers R.M., Myers R.M., Myers R.M., Smailus D.E., Marra M.A.; Marra M.A.; et than 15,000 full-length human	specific subsets of TISSUE SPECIFICITY. 0.1038/nn815; O'Donnell D., Roy MO., Pelletier M., Labarre M., Pelletier M., Payza K., a new family of sensory	S AA. date) ember X3 (Sensory neuron- ember K3 (Sensory neuron- ember K3 (Sensory neuron- ember K3 (Sensory neuron- ember K3 (Sensory neuron-	Q7tn44 rattus norv Q75xu5 gallus gall Bac87782 gallus ga Q9g2q6 homo sapien P01538 viscum albu Q9hbh6 homo sapien Q96h14 homo sapien Q9f180 neisseria m Q9fy88 neisseria m Q9fy98 neisseria m Q711n2 mus musculu Cac86130 mus musculu Cac86130 mus catesb Q7zu47 rana catesb

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EMBL; AF474987; AAL86878.2; --
EMBL; BC067292; AAH67292.1; --
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the European Bioinformatics Institute. The
use by non-profit institutions as a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Polymorphism; Transmembrane.
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FUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Potently activated by enkephalins (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeminal sensory neurons.
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RIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPE
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                         IAWLVFLCVVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFS
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D - W (in dbSNP:4274188).
FTId=VAR 019434.
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Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Male J.A., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley B. M. Townshman, I.W. Green E.D. Dickeon M. C.
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC067292; AAH67292.1; -.
Receptor.
SEQUENCE 322 AA; 36479 MW; B91DC082B6D95DA8 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-coupled receptor MRGX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                  278
263
                                                                                                                                                                            218
                                                                                                                                                                                                                                                                                                   158
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                                     LNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDTPEVDEGGG 321
                                                                                                                                                LCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSA
                                                                                                                                                                                                                                           CVLLWALSLLRSILEWMFCDFLFSGADSVWCETSDFITIAWLVFLCVVLCGSSLVLLVRI
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                                                                                                                LCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSA
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 224; DB
; Pred. No. 9e-
0; Mismatches
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RESULT 3 SNS2_HUMA

HUMAN

SNS2 HUMAN Q8TDE0; 01-OCT-2004

STANDARD;

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45, Created)

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Query Match
Best Local 9
 Matches
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                                                                                                                                                                                                                  TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Proenkephalin A gene products activate a new family of sensory neuron-specific GPCRs.";
Nat. Neurosci. 5:201-209 (2002).

-i-FUNCTION: Orphan receptor. Probably involved in the function nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lembo P.M.C., Grazzini E., Groblewski T., O'Do
Zhang J., Hoffert C., Cao J., Schmidt R., Pell
Gosselin M., Fortin Y., Banville D., Shen S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=21853733; PubMed=1185634; DOI=10.1038/nn815; Lembo P.M.C., Grazzini B., Groblewski T., O'Donnell D., R Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., I Gosselin M., Fortin Y., Banville D., Shen S., Stroem P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Sensory neuron-specific G-protein coupled receptor
                                                                                                                                                                                                                                                                                                PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=SNSR2;
Homo sapiens (Human).
                                                     SEQUENCE
                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF474988; AAL86879.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dray A., Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                DOMAIN
                                                                                                                       TRANSMEM
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                                                                                                            DOMAIN
                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                              send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potently activated by enkephalins (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: Uniquely localized in a subset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              root and trigeminal
                                                                                                                                                                                                                                                                                                                                         PF00001; 7tm_1; 1
 86;
                                                                                                                                                                                                                                                                                                                                                                                              an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subfamily.
               Similarity
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54
61
82
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118
141
162
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                                                                                                                                                            1 receptor;
32
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96
117
140
1161
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Primates;
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            25.5%;
                                                      36594
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 0:
                                                                                                                                                                                                                                                                       Transmembrane.
Extracellular (Potential)
               Score 86;
Pred. No.
                                                                  Cytoplasmic (Potential).
N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                 Cytoplasmic 2 (Potential
                                                                                               Extracellular (Potential).
7 (Potential).
                                                                                                                      Cytoplasmic 6 (Potential
                                                                                                                                                            Extracellular (Potential)
                                                                                                                                                                                        Cytoplasmic
                                                                                                                                                                                                                 Extracellular (Potential).
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                                                     D8C24308E3B4611B CRC64;
                                                                                            (Potential)
                                                                                                                                                  (Potential)
                                                                                                                                                                           (Potential)
                                                                                                                                                                                                      (Potential)
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                                                                                                                                                                                                                                                           (Potential)
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
1.7e-76;
hes 0;
                          DB 1;
                                                                                                                                                                                                                                             (Potential).
                                                                                                                                                                                      (Potential).
                                                                                                                                    (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in a subset of small dorsal
                         Length 322;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy M. -0.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Payza K.,
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204 VVLCGSSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKV 263

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RESULT
MRG1_H
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member X1
specific G-protein coupled receptor 4).
Name=MRGX1; Synonyms=SNSR4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto Tsutsumi S., Aburatani H., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Suwa M., Sato T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeda S., Kadowaki S., Haga T., Take "Identification of G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Proenkephalin A gene products activate neuron-specific GPCRs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21853733; PubMed=11850634; DOI=10.108/mn815; Lembo P.M.C., Grazzini E., Groblewski T., O'Donnell D., Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M., Gosselin M., Fortin Y., Banville D., Shen S., Stroem P.
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Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson
M. diverse family of GPCRs expressed in specific subs
nociceptive sensory neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett.
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                                                                                                                                                                                                                                                                                                                                       FUNCTION: Orphan receptor. Probably involved in the function of nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Potently activated by enkephalins including BAM22 (bovine adrenal medulla peptide 22) and BAM (8-22). BAM22 is the most potent compound and evoked a large and dose-dependent release of intracellular calcium in stably transfected cells. G(alpha)q proteins are involved in the calcium-signaling pathway. SUBCELIULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeminal sensory neurons.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                 Mas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence."
                                                                                                                                                                                                                                                                                                                 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22040266; PubMed=12044878;
3., Kadowaki S., Haga T., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walker P., Ahmad S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFCHVHLVSIFLSALNSSANPIIYFF
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pled receptor genes
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send an email to license@isb-sib.ch).

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QBTDD9;
01-OCT-2004
01-OCT-2004
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VARIANT
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PROSITE; PS00237; G PROTEIN RECEP F1
PROSITE; PS50262; G PROTEIN RECEP F1
G-protein coupled receptor; Glycoprol
DOMAIN 1 31 Extrace
                                                                                                                                       SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=21853733; PubMed=11850634; DOI=10.1038/nn815;
Lembo P.M.C., Grazzini E., Grobleweki T., O'Donnell D.,
Zhang J., Hoffert C., Cao J., Schmidt R., Pelletier M.,
                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                        01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-CCT-2004 (Rel. 45, Last amotation update)
Sensory neuron-specific G-protein coupled receptor 3.
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                                                                                           "Proenkephalin A gene products activate a new neuron-specific GPCRs.";
                                                                                                                 Gosselin M., Fortin Y., Banville D., Shen S., Dray A., Walker P., Ahmad S.;
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                                                     . Neurosci. 5:201-209(2002).
FUNCTION: Orphan receptor. Probably involved nociceptive neurons. May regulate nociceptor.
          development, including the sensation or modulation of pain. Potently activated by enkephalins including BAM22 (bovine adrenal medulla peptide 22) and BAM (8-22). BAM22 is the most potent compound and evoked a large and dose-dependent release of
                                                                                                                                                                                                                                                                                                                                                                                          263 VLFCHVHLVSIFLSALNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQD
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AF474990;
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calcium in stably
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N-linked (GlcNac...) (Pot.
I -> V (in dbSNP:11024885).
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2 (Potential).
Extracellular (Potential)
3 (Potential).
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/FTId=VAR_019432.
I -> V (in Ref. 2
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7 (Potentia
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Labarre M.,
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Matches 44
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MRG4 HUMAN
Q96LA9; Q8TDI
01-OCT-2004
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01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member
specific G-protein coupled receptor 6).
Name=MRGX4; Synonyms=SNSR6;
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DOMAIN
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF474989; AAL86880.2; -. InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest
                                   Dong X., Han S.-K., Zylka M.J., Simon WA diverse family of GPCRs expressed nocloeptive sensory neurons."; Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                      MEDLINE=21435808; PubMed=11551509;
Dong X., Han S.-K., Zylka M.J., Si
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                        Homo sapiens
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           EQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins are involved in the calcium-signaling pathway. SUBCELULIAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: Uniquely localized in a subset of a root and trigeminal sensory neurons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mas subfamily.
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                                                                                                                                                                                                                                                        STANDARD;
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., AND TISSUE SPECIFICITY.
PubMed=11850634; DOI=10.1038/nn815;
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0; Mismatches
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N-linked (G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential)
7 (Potential).
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                                                                        Simon
                                                          n M.I.,
in spec
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1e-34;
                                                            specific
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                                                                       Anderson D.J.;
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MBL outstation -
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Best Local
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                 PROSITÉ; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITÉ; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G_PROTEIN_GENERAL POLYMORPHISM; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lembo P.M.C., Grazzini E.,
Zhang J., Hoffert C., Cao
Gosselin M., Fortin Y., Ba
Dray A., Walker P., Ahmad
                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Proenkephalin A gene products activate a new neuron-specific GPCRs.";
                                                                                                                                                      VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potently activated by enkephalins (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUB SPECIFICITY: Uniquely localized in a subset of small dorsal root and trigeminal sensory neurons.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Neurosci. 5:201-209(2002).
FUNCTION: Orphan receptor. Probably involved nociceptive neurons. May regulate nociceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mas subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nociceptive neurons. May regulate nociceptor function development, including the sensation or modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         607230;
194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AY042216; AAK91807.1; -. AF474992; AAL86883.1; -.
                                           41;
                                                      Similarity
            SSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGI
SSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR000276; GPCR_Rhodpsn
                                                                                   182
319
322
                                           Conservative
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                                     12.2%; 500
100.0%; Pr
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                                                                                      Œ;
                                                    Score 41;
Pred. No.
                                                                                                                                                                                                          Cytoplasmic (Potential).
N-linked (GlcNAc...) (
N-linked (GlcNAc...)
                                                                                                                                          Extracellular 5 (Potential).
                                                                                                                                                                                                                                                                                                                Cytoplasmic 4 (Potential
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2 (Potential).
Extracellular (Potential).
3 (Potential).
                                                                                                                                /FTId=VAR_019437.
S -> L (in dbSNP:2445179)
                                                                                                                                                                                                                                                 Extracellular (Potential).
7 (Potential).
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                                                                                                                                                                                      F -> L (in dbSNP:2468774).
/FTId=VAR_019435.
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                                                                                 -> V (in Ref. 2).
-> K (in Ref. 2).
7CA676F8BD390A31 CRC64;
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                                           Mismatches
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RESULT 7

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01-OCT-2004
01-OCT-2004
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TRANSMEM
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01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Sensory neuron-specific G-protein coupled receptor
                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            G-protein coupled DOMAIN 1
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1 1;

PROSITE; PS50562; G PROTEIN RECEP_F1 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Proenkephalin A gene products activate a new family of sensory neuron-specific GPCRs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurosci. 5:201-209(2002)
FUNCTION: Orphan receptor. Probably involved nociceptive neurons. May regulate nociceptor development, including the sensation or modul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potently activated by enkephalins (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUB SPECIFICITY: Uniquely localized in a subset
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                                                            Similarity
    SSLVLLVRILCGSRXMPLTRLYVTILLTVLVFLLCGLPFGI 249
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322 AA;
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Belongs to family 1 of G-protein coupled receptors.
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100.0%; Pr
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                                                            Score 41;
Pred. No.
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                                                                                                                        3D6FFB4B5DDFDD90 CRC64;
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BB
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                                                                                Length 322;
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Labarre M.,
Payza K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function
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RESULT 8
MRG2_HUMAN
ID _MRG2_H
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Stapleton M., Godein T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
RGeneration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
                                                                                                    ganglion.";
J. Biol. Chem.
-!- FUNCTION: O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2004
01-OCT-2004
01-OCT-2004
                                                                                                                                                                        PubMed=12915402; DOI=10.1074/jbc.M302456200; Robas N., Mead B., Fidock M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Suwa M., Sato T., Okouc
Tsutsumi S., Aburatani
"Genome-wide discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome sequence.
FEBS Lett. 520:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nociceptive sensory neurons.";
Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dong X., Han S.-K., Zylka M.J., Simon "A diverse family of GPCRs expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21435808; PubMed=11551509;
Dong X., Han S.-K., Zylka M.J., Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=MRGX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96LB1;
                                                                                                                                                          "MrgX2 is
                                                                                                                                                                                                           TISSUE SPECIFICITY, AND POSSIBLE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mas-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takeda S., Kadowaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=
nociceptive neurons. May regulate nociceptor function and/or development, including the sensation or modulation of pain. Cortistatin-14 seems to be a high potency ligand at this receptor. Cortistatin has several biological functions including roles in sleep regulation locomotor activity, and cortical function. In receptor-expressing cells, cortistatin-stimulated increases in
                                                                                                      FUNCTION: Orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
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                                                                                                                                                      a high potency
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(Rel.
(Rel.
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                                                                                                                                                                   , œ.
                                                                                                                      278:44400-44404 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okouchi I., Arita M., Futami K., Matsumoto S., atani H., Asai K., Akiyama Y.; overy and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12044878;
Fi S., Haga T., Takaesu H., Mitaku S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                    receptor. Probably involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
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                                                                                                                                                        cortistatin receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                    function on and/or
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                                                                                                                                                          dorsal root
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RESULT 9 AAH63450

RRN OCC GREDT DAC

Homo sapiens

(Human)

Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.

protein-coupled

receptor

, Last Last MRGX2.

Last annotation

update)

sequence update)

Created)

02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,

AAH63450;

PRELIMINARY;

8

Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;

SEQUENCE FROM TISSUE=Brain;

N.A.

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Best Local S
Matches 20
                                                                                                                                                                                                                 DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                 G-protein
                                                                                                                                                                                                                                                                                          PRINTS; PR00237; GFCRRHODOPSN PROSITE; PS00237; G_PROTEIN_RI PROSITE; PS50262; G_PROTEIN_RI
                                                                                                                                                                                                                                                                                                                                                        EMBL; AY042214; AAK91805.1; -.
EMBL; AB063626; BAB89339.1; -.
EMBL; AB0656811; BAC06030.1; -.
EMBL; BC063450; AAH63450.1; -.
                                                                                                                              TRANSMEM
                                                                                                         VARIANT
                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                            Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                     nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coupled.
SUECELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Has a limited expression pro
peripheral and within the central nervous system
levels in dorsal root ganglion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mas subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to family 1 of G-protein coupled receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intracellular Ca(2+) but had no effect on bas
stimulated cAMP levels, suggesting that this
                                                                                                                                                                                                                                                                                                                                               607228;
224
                     232
                                                    Similarity
                    TILLTYLYFLLCGLPFGIQW 251
TILLTVLVFLLCGLPFGIQW
                                                                                                                                                                                                                                                                                coupled
                                                                                                                                                                                                                                                                                                                                    IPR000276; GPCR_Rhodpsn
                                                                                    330
                                                                                                        Conservative
                                                                                    AA;
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G_PROTBIN_RECEP_F1_2; 1.

G_PROTBIN_RECEP_F1_2; 1.

receptor; Polymorphism; Transmembrane.

33 Extracellular (Potential).
                                                                                                         37099 MW;
                                                   5.9%;
                                         <u>.</u>
                                                               Score 20;
                                                                                                         Cytopl
                                                                                                                               Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential)
7 (Potential).
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Extracellular (Potential)
5 (Potential).
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2 (Potential).
Extracellular (Potential)
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                                                                                                                                                                                                                                                              1 (Potential).
243
                                                    Pred. No.
                                                                                                                                                                                                                   (Potential)
                                                                                     0B328FD78B1DF6BE CRC64
                                           Mismatches
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                                                    DB 1; Le
7.6e-11;
                                                                                                                    (Potential)
                                                                                                                                                                                                       (Potential).
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s system, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       basal
                                                               Length 330;
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ptor is G(q)
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MGA3_MOUSE
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                  EQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RESTRAIN-C578L/6; TISSUE-Borsal root ganglion;

RESTRAIN-C578L/6; TISSUE-Borsal root ganglion;

REDLINE-21435808; PubMed-11551509;

REDLINE-21435808;

REDLINE-2143580
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01-OCT-2004
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01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member
Name=Mrgpra3; Synonyms=Mrga3;
Mis musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria;
NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
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                                                                                       subfamily.
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Rodentia;
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Pred. No.
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7.6e-11;
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RESULT
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Matches 15
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01-OCT-2004
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TRANSMEM
DOMAIN
                                                                                                                                                  "A diverse family of GPCRs expressed in spec nociceptive sensory neurons."; Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
SEQUENCE
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS00237; GFROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             SEQUENCE FROM N.A., SUBCELLULAR LO STRAIN=C57BL/6; TISSUE=Dormal root MEDLINE=21435808; PubMed=11551509;
                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                       Name=Mrgpral; Synonyms=Mrgal;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                               coupled receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGA1_MOUSE
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InterPro; IPR000276; GPCR_Rhodpsn.
Dfam. PF00001; 7tm_1; 1.
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                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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FUNCTION: Orphan receptor. May be a receptor for RFamide-family neuropeptides such as NPFF and NPAF, which are analysesic in vivo May regulate nociceptor function and/or development, including t sensation or modulation of pain.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that includes nociceptors. Expressed in the subclass of nonpeptidergic sensory neurons that are IB4(+) and VR1(-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GLSMLSAISTERCLS 138
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302 /
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17 Extracellular (Potential).
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Extracellular (Potential).

3 (Potential).

4 (Potential).

4 (Potential).

5 (Potential).

Extracellular (Potential).

5 (Potential).

6 (Potential).

6 (Potential).

7 (Potential).

Extracellular (Potential).

8 (Potential).

Cytoplasmic (Potential).

N-linked (GloNAC. ...) (Potential).

N-linked (GloNAC. ...) (Potential).

N-linked (GloNAC. ...) (Potential).
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Cytoplasmic (Potential).
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                           .I., Anderson D.J. specific subsets
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                           ry neurons that nonpeptidergic
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Best Local S
Matches 15
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Q7TN49;
01-OCT-2004
01-OCT-2004
01-OCT-2004
                                                                                               STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
MEDLINE=22810130; PubMed=12909716; DOI=10.1073/pnas.1732949100;
                                                                                                                                                                                                                     01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member A.
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CARBOHYD
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DOMAIN
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                                                                   protein-coupled receptor family.";
Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
                                                                                          Zylka M.J., Dong X., Southwell A.L., Anderson D.J.; "Atypical expansion in mice of the sensory neuron-specific Mrg
                                                                                                                                                                                               Name=Mrgpra; Synonyms=Mrga;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrane.
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                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                FUNCTION: Orphan receptor. May regulate nociceptor function and/or development, including the sensation or modulation of pain. SUBCELLULAR LOCATION: Integral membrane protein.
             Mas
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                     SIMILARITY: Belongs to
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             subfamily.
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100.0%; Pr
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Pred. No.
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Extracellula
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N-linked (GlcNAc
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6 (Potential).
Extracellular (Potential).
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  (See http://www.isb-sib.ch/announce/
                    G-protein
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                      coupled receptors
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RESULT 13
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Best Local
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Q91ZC5;
01-OCT-2004
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SEQUENCE
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TRANSMEM
DOMAIN
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01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member
Name=Mrgpra7; Synonyms=Mrga7;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
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TRANSMEM
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RGD; 738050; Mrgpra.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR00027; G_PROTEIN_RECEP_F1
PROSITE; PS00237; G_PROTEIN_RECEP_F1
PROSITE; PS50262; G_PROTEIN_RECEP_F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                         ÷
                                                                                                                                                        MEDLINE=21435808; PubMed=11551509;
Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.
"A diverse family of GPCRs expressed in specific subsets
nociceptive sensory neurons.";
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                     May regulate nociceptor function and/or development, including the sensation or modulation of pain (By similarity).
SUBCELLULAR LOCATION: Integral membrane protectin.
TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that includes nociceptors. Expressed in the subclass of nonpeptidergic sensory neurons that are IB4(+) and VR1(-).
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                FUNCTION: Orphan receptor. May be a receptor for RFamide-family neuropeptides such as NPFF and NPAF, which are analgesic in viv
                                                                                                                                          106:619-632 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GLSMLSAISTERCLS
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             subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equires a license agreement (S email to license@isb-sib.ch).
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Extracellular (Potential).

5 (Potential).

Cytoplasmic (Potential).

6 (Potential).

Extracellular (Potential).

7 (Potential).
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Pred. No.
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1 (Potential).
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4A820A4E0192E8B6 CRC6
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Cytoplasmic (
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2 (Potentia
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Best Local S
Matches 15
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Q91ZC4;
01-OCT-2004
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TRANSMEM
DOMAIN
                                                                                                                                                                                                                                   MEDLINE=21435808; PubMed=11551509;
MEDLINE=21435808; PubMed=11551509;
Han S.-K., Zylka M.J., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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                                                                                                                                                                                                    nociceptive sensory neurons.";
Cell 106:619-632(2001).
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
[1]
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                                   FUNCTION: Orphan receptor. May be a receptor for RFamide-family neuropeptides such as NPFF and NPAF, which are analgesic in vivo. May regulate nociceptor function and/or development, including the sensation or modulation of pain (By similarity).

SUBCELULIAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that includes nociceptors. Expressed in the subclass of nonpeptidergic sensory neurons that are IB4(+) and VR1(-).
                  includes nociceptors. Exp
sensory neurons that are
SIMILARITY: Belongs to fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GLSMLSAISTERCLS 138
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 45, Created)
(Rel. 45, Last sequence update)
(Rel. 45, Last annotation update)
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Rodentia;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                     and VR1(-).
of G-protes
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                     G-protein coupled receptors
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hes 0;
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subsets of
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Best Local :
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2004 (Rel. 45, Created)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Mas-related G-protein coupled receptor member A4
                                                                                                                Dong X., Han S.-K., Zylka M.J., Simon M.I., Anderson D.J.
"A diverse family of GPCRs expressed in specific subsets
nociceptive sensory neurons.";
Cell 106:619-632(2001).
                                                                                                                                                                                            SEQUENCE FROM N.A., SUBCELLULAR LOCATION, STRAIN=C57BL/6; TISSUE-Dorbal root gangli MEDLINE=21435808; PubMed=11551509;
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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PROSITE; PS00237; GFROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                             Name=Mrgpra4; Synonyms=Mrga4;
                                                                                                                                                                                                                                                                                                                                                                                  coupled receptor)
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
FUNCTION: Orphan receptor. May be a receptor for RPamide-family neuropeptides such as NPFF and NPAF, which are analgesic in vivo May regulate nocliceptor function and/or development, including tsensation or modulation of pain.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed in a subset of sensory neurons that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
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Rodentia;
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Pred. No.
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w-linked (GLCWAc. . .) (Potential).
w-linked (GLCWAc. . .) (Potential).
closes continuous contin
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5 (Potential).
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Extracellular (Potential)
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7 (Potential).
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Search completed: October 27, 2004, 08:51:36 Job time : 197 secs
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY042194; AAK91790.1; -.
MGD; MGI:3033100; MTGDra4.
InterPro; IPR000276; GPCR Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            TRANSMEM
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SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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0; Mismatches 0;
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N-linked (GLONAc. . .) (Potential).
N-linked (GLONAc. . .) (Potential).
; 22F3AEC2F2F7127B CRC64;
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7 (Potential)
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Listing first 45 summaries
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
20, Appl	18282, 7	1, Appli	1, Appla	16, App	10, App	17, App	16, App	134, Apr	222, App		219, App		73, App	5, Appli	25490, 1	1, Appli	26, App1

ALIGNMENTS

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; SEQ ID NO 4
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-254-227A-4
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APPLICANT: Banville, Denis
APPLICANT: Benville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
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GENERAL INFORMATION:
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Best Local Similarity
Matches 957; Conserv
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GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC
                       GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC
                                                                                ATATTTTCGCCGTTACCCCTCATCAATATCCGCCATCCCAACTCCCAAAATCCTCAGTCCT
                                                                                                          ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCCATCTCCAAAAATCCTCAGTCCT
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Sequence 6, Application US/09254227A

| Patent No. 6696257
| GENERAL INFORMATION:
| APPLICANT: Ahmad, Sultan
| APPLICANT: Banville, Denis
| APPLICANT: Benville, Denis
| APPLICANT: Fortin, Yves
| APPLICANT: Lembo, Paola
| APPLICANT: Combonell, Dajan
| APPLICANT: Shi-Hsiang, Shen
| TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat
| FILE REFERENCE: 81823/268117
| CURRENT APPLICATION NUMBER: US/09/254,227A
| CURRENT FILING DATE: 1999-03-03
| NUMBER OF SEQ ID NOS: 22
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 6
| LENGTH: 969
| TYPE: DNA
| ORGANISM: Homo sapiens
| US-09-254-227A-6
                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-254-227A-6
            Query Match 35.9%;
Best Local Similarity 98.0%;
Matches 950; Conservative
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            Score 938.6; DB 4;
Pred. No. 3.7e-260;
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; SEQ ID NO 12
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US-09-254-227A-12
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Best Local Similarity 91.4%;
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AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG 1271
                                                    ACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGGCCCCTGTTTTCC
                                                                                                        AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC 115:
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Pred. No. 1.2e-230;
0; Mismatches 83;
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Best Local Similarity
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APPLICANT: Banville, Denis
APPLICANT: Portin, Yves
APPLICANT: Lembo, Paola
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Haiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
RUMBER OF SEQ ID NOS: 22
RUMBER OF SEQ ID NOS: 22
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Pred. No. 1e-229;
0; Mismatches 85; Indels
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RESULT 5
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SEQ ID NO 14
LENGTH: 969
TYPE: DNA
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Patent No. 6696257
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Best Local Similarity
Matches 882; Conserv
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APPLICANT: Banville, Denis
APPLICANT: Borville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: Commell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
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Pred. No. 8.6e-229;
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Sequence 10, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
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APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Haiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
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Best Local Similarity 90.8%;
Matches 880; Conservative
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TYPE: DNA
ORGANISM: Homo sapiens
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TCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 1331
                                                                                                                                       ACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCC 121:
                                                                                                                                                                                                    AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTC
                                                                                                                                                                                                                                                                 AICGCGIGGCIGGTITITITATGIGIGGTICCTCIGIGGGCCCAGCCIGGTCCIGGIC 1091
                                                                                                                                                                                                                                                                                                                                TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA 1031
                                                                                                                                                                                                                                                                                                                                                                               GTGGTGTGTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGGAGCATCCTGGAGTGGATGTTA 480
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                                                                        AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTTCCAGTTTTTCCTG
                                                                                                                   ACAGTACTGGTCTTCCTCTCTGTGGCCTGTCGCATTCAGTTTTTCCTATTTTTA 720
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Pred. No. 7.2e-228;
0; Mismatches 89;
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SOFTWARE: Pat.
SEQ ID NO 2
LENGTH: 1011
TYPE: DNA
ORGANISM: rat
US-09-254-227A-2
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US-09-254-227A-2
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Best Local Similarity
Matches 655; Conserv
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APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
TITLE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                       TCCTGGTCCCCATCATCACCCTGCTTGGATTGGCAGGAAACACCATTGTACTCTGGCTCT 193
                                                                                                                                                                                                                                                                                                                                                                                                          CTACAACACTGAATAAAACTGGTCA---TCCCAGTTGCAGGCCAATCCTCACCCTGTCCT 133
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CAATCTGGTACCACTGCCACCGCCCAAGAAACATGTCAGCTATTATATGTGTTCTAATCT
                     TGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGGCCG
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                                                                                    TTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.7%;
ilarity 65.6%;
Conservative
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Pred. No. 8.4e-108;
0; Mismatches 323;
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APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GEN
FILE REFERENCE: PA-0013 US
CURRENT APPLICATION NUMBER: US/09/495,050A
CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 164
LENGTH: 291
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US-09-495-050A-164
; Sequence 164, Application US/09495050A
; Patent No. 6492505
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                                                                                                                                                              Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6492505 1909132CT1
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AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC
                                                                                                       CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA
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                                                                                                                                               Conservative
                                                                                                                                             11.1%; Score 291; DB 4; 1 100.0%; Pred. No. 8.5e-74; tive 0; Mismatches 0;
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US-09-016-434-330
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                                                                                                                                                                  Query Match
                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 330,
                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING TITLE OF INVENTION: PATHWAY GENE EXPRESSION NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEB: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                           TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 ELECTRIC (650)
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                                                                                                                                                                                                                       CLONE: 1909132
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STATE: CALIFORNIA
                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                          762 CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA 821
                                                                                                                                275;
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                                                                                                                                                 Similarity
AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGFAC
                                                      CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCCTACTTTATAGGCCTA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTA
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                                                                                                                              10.5%; Score 275; DB 4; I ilarity 100.0%; Pred. No. 3.4e-69; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                            CONNTUTOI
                                                                                                                                                                                                                                                                              linear
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ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (148567)
OTHER INFORMATION: n = A,T
US-09-801-876B-3
; Sequence 3, Application US/10254869
patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN K
; TITLE OF INVENTION: ACID MOLECULES
; TITLE OF INVENTION: THEREOF
                                                                                                                                     RESULT 11
US-10-254-869-3/c
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US-09-801-876B-3/c
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Matches
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APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01160
CURRENT APPLICATION NUMBER: US/09/801,876B
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09801876B Patent No. 6492155
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Best Local Similarity
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SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                             AGGCCTCCCCAGAAGCAGAAGCTGCTATGCTTTGTACAGTCTGTAGAGCTATTAGCCA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCACCATGTGAGATGCCCTGCTCCCCTTTTTGCCTTCCACAATGATTGGAAGCTTCCTG 50380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCACCATGTGAGACGCCTCGCTCCCC-CTTTGCCTTTCACCAGGATTGGAAGCTTCCTG 142
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                                                                                                                                                                                                                                                                                            CTTAAACTTCTTTTCTTTAAAAATTACCCAGTCTCAGGTATTTCTTTATAGCAATGTGAG
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 ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PITHEREOF
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Pred. No. 2.7e-30;
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RESULT 12
US-09-022-461-1
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CURRENT FILING DATE: 2002-09-26
NUMBER OF SEQ ID NOS: 8
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 148567
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(148567)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                               CTTAAACTTCTTTTTTTTTAAAAATTACCCAGTCTCAGGTATTTCTTTATAGCAATGTGAG 50261
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                                                                                                                                                                                                                                                                                                                                CTCACCATGTGAGACGCCTCGCTCCCC-CTTTGCCTTTCACCAGGATTGGAAGCTTCCTG 142
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                                                                          AACTGACTAATACACTCACA 50241
                                                                                             AATGAACTAATACACAGACA 282
                                                                                                                                                                                                                     AGTCCTCCCCA-AAGCAGAAGCCACTATGCTTCCTGCACAGCCTGCAGAACCATGAGCCA
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80.4%;
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Pred. No. 2.7e-30;
0; Mismatches 46
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COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.
CURRENT APPLICATION DATA:
*DOLICATION NUMBER: US/09/022,461 Sequence 1, Application US/09022461 Patent No. 5964371 GENERAL INFORMATION: CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/900
APPLICATION NUMBER: 08-900
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Catherine, Polizzi I APPLICANT: APPLICANT: CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD TITLE OF INVENTION: PROST NUMBER OF SEQUENCES: APPLICANT: APPLICATION NUMBER: US/0 FILING DATE: 12-FEB-1998 STREET: 755 PAGI CITY: Palo Alto ß SCHUUR, Bric R. LAMPARSKI, Henry G. HENDERSON, Daniel R. YU, De Chao PROSTATE CANCER DRUG 08/906,192

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Applic Patent No. 6432700
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APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PITITLE OF INVENTION: FITITLE OF INVENTION: COUMBER OF SEQUENCES:
                                                                                                                                                                    ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                APPLICATION NUMBER: FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415.813-5600
              FILING DATE:
ATTORNEY/AGEN'INFORMATION:
NAME: Catherine, Polizzi M
REGISTRATION NUMBER: 40,130
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
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Local 189;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER:
                                                                                      APPLICATION NUMBER:
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ER: 34802-20003.21
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Pred. No. 6.2e-27;
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                                                                                                                                                                                                                                                                                SEQ ID NO 11
LENGTH: 12047
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09474699 Patent No. 6495130 GENERAL INFORMATION:
                                                                                                                                                                                                    Query Match 5.0%;
Best Local Similarity 75.9%;
                                                                                                                                                                                   Matches 189;
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Henderson, Daniel R.
APPLICANT: Yu, De Chao
IITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS
IITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF
FILE REFERENCE: 348022001300
CURRENT APPLICATION NUMBER: US/09/474,699
CURRENT FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/114,262
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 23
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 12047 base pairs
TYPE: nucleic acid
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TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
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TELEFAX: 706141
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TOPOLOGY: 111
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Pred. No. 6.2e-27;
0; Mismatches 58
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US-09-151-3/6-3

Sequence 3, Application US/09151376

Patent No. 6676935

GENERAL INFORMATION:

APPLICANT: Henderson, D.R.

APPLICANT: Schuur, E.R.

TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS

FILE REFERENCE: 348022000221

CURRENT APPLICATION NUMBER: US/09/151,376

CURRENT APPLICATION NUMBER: 08/669,753

EARLIER APPLICATION NUMBER: 08/495,034

EARLIER FILING DATE: 1996-06-26

EARLIER APPLICATION NUMBER: 08/495,034

EARLIER APPLICATION NUMBER: 08/495,034

EARLIER APPLICATION NUMBER: 08/495,034

EARLIER APPLICATION NUMBER: 08/495,034

EARLIER PILING DATE: 1995-06-27

NUMBER OF SEQ ID NOS: 71

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 3

LENGTH: 12047

TYPE: DNA

ORGANISM: Homo sapiens
Search completed: October 29, 2004, 16:11:07 Job time : 220 secs
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                                                                                      5558 ACTANTACA 5566
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications NA:*

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Gapop 10.0 , Gapext 1.0
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2618
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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100.0 58.4 45.6 42.2 41.8 41.8 40.2 39.7 39.7 38.7	Query Match
2618 1997 2040 1369 8622 1400 1400 1370 1369 1369 1604	Query Match Length
114 115 115 115 115 115	DB
US-09-867-570-1 US-10-219-834-7 US-10-183-116-15 US-10-292-798-1273 US-09-867-570-3 US-10-183-116-30 US-10-292-567A-673 US-10-017-161-1599 US-10-017-161-1055 US-10-292-798-897 US-10-183-116-32 US-10-183-116-32 US-10-225-567A-688	ID
Sequence 1, Appli Sequence 7, Appli Sequence 15, Appli Sequence 1273, Appli Sequence 3, Appli Sequence 30, Appli Sequence 673, Appli Sequence 673, Appli Sequence 1559, Appli Sequence 1055, Appli Sequence 897, Appli Sequence 897, Appli Sequence 688, Appli	Description

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608.8	608.8	608.8	608.8	608.8	618.8	628.8	687.8	713.8	740.2	755.4	769.6	787.4	792.2	٠	823.2	829.8	829.8	829.8	829.8	829.8	829.8	829.8	833	833	833	845.8	856.2	64	965.8	969	969	1012.2
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US-10-292-798-895	US-10-017-161-1053	US-10-225-567A-648	US-10-183-116-17	50-3	0-240-998-	US-10-072-012-175	0-017-161-	0-292-798-	US-10-292-798-1077	US-10-101-510-239	9	US-10-072-012-169	US-10-240-998-9	US-10-072-012-177	US-10-072-012-173	US-10-314-048A-19	US-10-321-807-19	US-10-343-650A-43	US-10-237-467-11	US-10-321-807-19	US-10-240-998-3	US-10-079-384-3	US-10-237-467-3	US-09-995-225-17	US-09-995-225-17	US-10-237-467-9	US-10-072-012-171	US-10-391-074-1	US-10-401-397A-1	US-09-995-225-19	US-09-995-225-19	US-10-292-798-1041
895, 1	1053,	648,	*	11,	7,	175, /	131	•	1077,	239	6, Ar	169	Sequence 9, Appli	177	e 173,	19, 7	19,	43,	11,	19,	ω	ω	3, 1	e 17	17	,	Sequence 171, App	_	Sequence 1, Appli	e 19,	19,	e 104

ALIGNMENTS

10. Application US/09867570 ion No. US20040076951A1 INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMATION: ISOLATED HUMAN G-PROTEIN COUPLED F INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR P INVENTION: RECEPTORS, NUD USES THEREOF FERENCE: CL000900-CIP APPLICATION NUMBER: US/09/867,570 FILING DATE: 2000-10-25 FILING DATE: 000-05 FILING DATE: 000-05 FILING DATE: 000-05 FILING DATE: 000-10-25	Q	B 8	B 8	Query Match Best Local Sim Matches 2618;	RESULT 1 US-09-867-570-1 Sequence 1, A Publication N GENERAL INFOR APPLICANT: W TITLE OF INV TITLE OF INV TITLE OF INV FILE REFEREN CURRENT APPL CURRENT APPL CURRENT FILING PRIOR FILING PRIOR FILING PRIOR FILING WIMBER OF SE SOFTWARE: FA SEQ ID NO 1 LENGTH: 261 TYPE: DNA ORGANISM: H US-09-867-570-1
DING HUMAN GPC 2618; 0; Gaps 0; Gaps CGTGTAGCACCT 6 CCCTTTGCCTTT 1 CCCTTTGCCTTT 1	121 CACCAGGATTGGAAGCTTCCTGAGGCCTCCCCAGAAGCAGAAGCTGCT		1 AACAATTGCCGCGAATTCGGCACGAGATGAAATCTAGTTGTTTAAAAG	100.0%; Score 2618; DB 11; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; I	pplicatio o. US2004 MATION: EI, Ming- ENTION: ENTION: CE: CL000 ICATION NUM MNG DATE: 20 Q ID NOS: stSEQ for 8
HUMAN GPC Gaps Gaps Gaps Gaps GapaccT 6 GACCACCT 6 GACCACCT 1 GCCTTT 1 TGCCTTT 1	ATGCT	CCC.	G=G	2618 0;	DING
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2281 GTAGGAGAATTCTTCATACTTCCAGGTTTTGTATAAATTGTTCTGATTGTAACTTTCAGT 2340 	2221 ATTTTAAAGTGGAAATTATCTTGAAAACCATTTATTATTCACTTACAGATTCTTTCAGTT 2280 	2161 TGAGGAGCCTATAAATATGTCCCACCAGTTTCATTTTGGCCATTGGAAACCTCAATATTG 2220		2041 CTGTCATTTGTCCACAGCATGGTGACATGTTGGCCTTGGTTTCTAGTAAAGACAATCGTG 2100	1981 GAGAGAGATTCTCCCTTCATAAAAACAGTCTTAGAAATTGGTTTTATGAATAGCCCTCTC 2040 	1921 GAGTICTGCTACCTCTAAATICCATIGAATICTCAGATATAAAGCAAAATAATGACCTTA 1980 	1861 TCATGTTCCCTTTTATGACTGGAGGCATTACTGCAGTTGGAAGCTCAATTCTTAATAAGT 1920 	1801 CCTGATAGTATCAAAAAGGAAGATTCCTTATTAATCTGTCAGACTATGTTCCCCTGAAAA 1860	1741 ATTGTAATAAAAGGAGTTGCTGTCCACAACCCTAAAACTCTTCTTTATACTTGTTTCCTA 1800		CACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGATTCTCCTTGATATTACCAAT		TGCTGCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCTCAGAAATG	GANGCAGATTIGGAGCAGTGAGGAAGAACCTCTGCCCCTGTCAGAACAAGAACTTTGAGAACAA	ACACGCCTGAGGTGGATGAAGGTGGAGGTTCCTCAGGAAACCCTGGAGCTGTCGGGTGGTTCGGGTGGAGGTGGAGCTGTCGGGAGGTGGAGGTGAACCCTGGAGGTGGAGGTGGAGGTGAACCCTGAAGGTGAAGGTTGAAGGTTGAAGGTTGGAGGTTCCTCAGGAAAACCCTGGAGGTGTCCTCCG	CTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGG	CCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTT CCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCT	

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Oy 462 TCATGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACA	Db 1453 TGCTGTCCACAACCCTAAAACTCTTCTTTATACTTTGTTTCCTACCTGATAGTATCAAAAA 1512 Qy 1818 GGAAGATTCCTTATTAATCTGTCAGACTATGTTCCCCTGAAAATCATGTTCCCCTTTATG 1877

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Sequence 1773, Application US/10292798

Publication No. US20030235833A1

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: AURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CCURRENT APPLICATION NUMBER: US/10/292,798
CCURRENT FILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PASTENTIAL Ver. 2.1
SEQ ID NO 1273
LENGTH: 1369
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US-10-292-798-1273
              TYPE: DNA ORGANISM: Homo sapiens
 FEATURE:
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Best Local Similarity
Matches 1195; Conser
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                                               ATTTACTTCCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTT
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Pred. No. 0;
0; Mismatches
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Sequence 3, Application US/09867570

Publication No. US20040076951A1

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MCLECULES ENCODING HUMA
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REPERENCE: CL000900-CIP
CURRENT APPLICATION NUMBER: US/09/867,570
CURRENT PAPLICATION NUMBER: 09/695,045
PRIOR APPLICATION NUMBER: 09/695,045
PRIOR APPLICATION NUMBER: 09/695,045
PRIOR FILING DATE: 2000-10-25

NUMBER: OF SEQ ID NOS: 4
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 8622
TYPE: DNA
ORGANISM: Human
US-09-867-570-3
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ilarity 99.6%;
Conservative
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Pred. No. 1.9e-300;
0; Mismatches 5;
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FILE REFERENCE: CALTE.4C1CP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR PILING DATE: 2000-08-01
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 09/849,869
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/10183116 Publication No. US20030092035A1
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; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FBSTESQ for Windows Ve
; SEQ ID NO 30
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: CDS
; LOCATION: (332)...(1297)
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Best Local Similarity 99.7%;
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                                       TGTCATGTGCATCTAGTTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATC
                                                                               CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTT
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APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR PILLING DATE: 2001-12-19
PRIOR PILLING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 673
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.6
Best Local Similarity 99.7
Matches 1096; Conservative
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US-10-017-161-1599

Sequence 1599, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION:

APPLICANT: SUWA, MAXIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAIN, HIROYUKI
TITLE OF INVENTION: NOTES OF PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT APPLICATION NUMBER: JD 2001/246789

PRIOR PILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PATENTIN SECTION 1599

LENGTH: 1370
TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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; NAME/KEY: CDS
; LOCATION: (996)..(1170)
US-10-017-161-1599
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Best Local Similarity 94.4%;
Matches 1136; Conservative
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Pred. No. 1.5e-286;
0; Mismatches 60;
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1369)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1169)
US-10-017-161-1055
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Publication No. US20030143668A1

GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152

CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT APPLICATION NUMBER: JE 2001/246789

PRIOR PILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430
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US-10-017-161-1055
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SEQ ID NO 1055
LENGTH: 1369
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Best Local Similarity 91.7%;
Matches 1100; Conservative
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                                                           ACGGTGCTGACGTGCATCGTTTCCCTTGTCGGGCTGACAGGAAACGCAGTTGTGCTCTGG
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CTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCG
                                                                                  ACGGGGCTGACGTGCATCGTTTCCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGG
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502 ACCTGACAGTTGCAGTTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGA 1660 	542 GCCTTCTGCCTCAGAAATGTCTCAGTGGTCCCTCAAGGTCTTCGAATAGATGTTTTATCTA 1601 	82 91	22 31	.362 CTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGAGGTGGAAGGTGGAGGGTGGCTTCCTCAG 1421	302 ATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTT 1361 	342 TGTCATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATC 1301 	B2 CCCTTIGGCAITCAGIGGGCCCIGITTICCAGGAICCACCIGGAITGGAAAGICITAITT 1241	122 CTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTG 1181	062 CTCTGTGGGTCCAGCCTGGTCCTGCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCG 1121	002 GTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGC	942 CTGCTGCGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT 1001	982 CACTGCCGCCCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCTCTGGGCCCTGTCC 941	322 AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC 881	62 CGCCATCCCATATATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA 821	02 GCCGACTTCCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATC 761	51

RESULT 10
US-10-292-798-897
; Sequence 897, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO

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APPLICANT: ANTENNA, TORMA

APPLICANT: ABURATANI, HIROYUKI

TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS

FILE REFERENCE: 084335/166

CURRENT APPLICATION NUMBER: US/10/292,798

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: 10/017,161

PRIOR FILING DATE: 2001-12-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070

SOPTWARE: Patentin Ver. 2.1

SEQ ID NO 897

LENGTH: 1369

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

LOCATION: SOURCE
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PRIOR FILLING DATE: 2000-08-01
PRIOR PELLICATION NUMBER: US 60/202,027
PRIOR FILLING DATE: 2000-05-04
PRIOR PELLICATION NUMBER: US 09/704,707
PRIOR PELLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR PILLING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
                                                                        SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 32
SENGTH: 1604
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT FILING DATE: 2002-06-26
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NUMBER OF SEQ ID NOS: 109
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                        AGAGGGCTCTGCAGGACAAGCCTGAGGTGGATAAAGGTGAAGGGCAGCTTCCTGAGGAAA
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Pred. No. 2.4e-275;
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TGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTT
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APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTITLE OF INVENTION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
INVENTIAL OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 688
LENGTH: 1604
TYPE: DNA
CRGANISM: Homo sapiens
US-10-225-567A-688
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Best Local Similarity 91.0
Matches 1090; Conservative
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GCCGCCGCCCACACACCTGTCAGCGGTCGTGTGTGTCCTGCTCTGGGGCCTGTCCCTGC
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Pred. No. 2.4e-275;
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GENERAL INFORMATION: OSCIOLARIA
GENERAL INFORMATION: APPLICANT: SUWA, MAKIKO
APPLICANT: ASHA, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUNOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: US/10/296
PRIOR FILING DATE: 2001-2-18
PRIOR APPLICATION NUMBER: US/10/246789
PRIOR FILING DATE: 2001-6-18
NUMBER OF ENG UD NOS: 2070
SOFTWARE: PATENTIN Ver. 2.1
LEQ ID NO 1041
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US-10-292-798-1041
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                                 LENGTH: 1369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
 LOCATION: source FEATURE:
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US-10-292-798-1041
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Matches 1088; Conservative
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AGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAA 1425
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Query Match 37.0%; Score 969; DB 9; Length 969; Best Local Similarity 100.0%; Pred. No. 7.2e-263; Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0; Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0; G	ORDANISM: Artificial Sequence FEATURE: OTHER INFORMATION: No. US20020193584A1el Sequence US-09-995-225-19	, w P	FILING DATE: 2001-0: APPLICATION NUMBER: FILING DATE: 2001-0: FIGURE TO NOS: 67	FILING DATE: 2001-0 APPLICATION NUMBER: FILING DATE: 2001-0 APPLICATION NUMBER:	PRIOR PILICATION NUMBER: 60/282,032 PRIOR PILING DATE: 2001-02-20 PRIOR PILICATION NUMBER: 60/282,032 PRIOR PILICATION NUMBER: 60/282,158	FILING DATE: 2001-0 APPLICATION NUMBER: FILING DATE: 2001-0	PRIOR FILING DATE: 2000-11-27 PRIOR PILING DATE: 2000-12-12 PRIOR PILING DATE: 2000-12-12 PRIOR PILING DATE: 2000-12-12 PRIOR PILING DATE: 2007-12-12		REFERENCE: AREN- NT APPLICATION N NT FILING DATE: APPLICATION NUM	APPLICANT: Lowitz, Kevin P. APPLICANT: Pride, Cameron APPLICANT: Pride, Cameron TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G TITLE OF INVENTION: Receptors	GRUERAL INFORMATION: APPLICANT: Chen, Ruoping APPLICANT: Chu, Zhi Liang APPLICANT: Chu, Zhi Liang	RESULT 14 US-09-995-225-19 ; Sequence 19, Application US/09995225 ; Publication No. US2002010358481	Db 1315 ACCTGACAGTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTT 1369	125 GCGTTTCGCCTCAGAAATGTCTCAGTGGTAACTCAAGGTCTTCAAATAAAT	1195 GACCGGACTTTGAGAGCAACACTGTCCCTGCCACCCTTGACAATTACATGCGTTTTTTCTTA		Qy 1426 CCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCA 1481
RESULT 15 US-09-995-225-19 Sequence 19, Application US/09995225 Publication No. US20030139588A9 GENERAL INFORMATION: APPLICANT: Chen, Ruoping	Qy 1452 GAGCAGTGA 1460 Db 961 GAGCAGTGA 969	Qy 1392 GTGGATGAAGGTGGAGGTGGCTTCCTCAGGAAAACCCTGGAGCTGTCGGGAAGCAGATTG 1451	Qy 1332 CGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGAGACACGCCTGAG 1391	Qy 1272 TCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 1331	Qy 1212 AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG 1271	Qy 1152 ACAGIGCTGGICTTCCTCCTCTGTGGCCCTTTTGGCATTCAGTGGGCCCTGTTTTCC 1211	Oy 1092 AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC 1151	Qy 1032 ATCGCGTGGCTGGTTTTTTATGTGTGGGTTCTCTGTGGGTTCCAGCCTGGTCCTGCTGGTC 1091	Qy 972 IGTGACITCCIGITTAGIGGIGCTGAITCIGITIGGIGJGAAACGICAGAITTCAITACA 1031	Qy 912 GTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGAGTATCCTGGAGTGGÀTGTTC 971	Qy 852 TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCGCCCAGATACCTGTCATCG 911	Qy 792 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 851	OY 732 ATATGITCGCCGTTACGCCTCATCAATATCCGCCATCCCAAAATCCTCAGTCCT 791	Qy 672 GTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCTCTCCTTAGCGGCCACATT 731	Qy 612 GCGCTGACAGGAAACGCGGTTGTGCTCTGGGCTGCCGGCATGCGCAGGAACGCT 671	Qy 552 ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC 611	Db 1 ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 60

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612 121 672 181 732 241 792 301	Query Match 37.0%; Score 969; DB 10; Best Local Similarity 100.0%; Bred. No. 7.2e-26 Matches 969; Conservative 0; Mismatches 0 492 ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGAC	APPLICANT: Chu, Zhi Liang APPLICANT: Dang, Huong T. APPLICANT: Pride, Cameron TITLE OF INVENTION: Endogenous And No. TITLE OF INVENTION UNMBER: US/09/995,2 TRIOR APPLICATION NUMBER: 60/253,404 PRIOR APPLICATION NUMBER: 60/253,404 PRIOR APPLICATION NUMBER: 60/270,286 PRIOR APPLICATION NUMBER: 60/270,286 PRIOR APPLICATION NUMBER: 60/282,365 PRIOR APPLICATION NUMBER: 60/282,356 PRIOR APPLICATION
	Length 969; ; Indels 0; Gaps 0; ACCAATCAACGGACGTGAGGAG 551 ACCAATCAACGGACGTGAGGAG 60 GACGTGCATCGATCGTTCCCTTGTC 611	US20030139588A9-Endogenous Versions of Human
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3 960	GTGGATGAAGGTGGAGGGTTCCTCAGGAAACCCTGGAGCTGTCGGGAAGCAGATTG	901	망
3 145	GTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCCTGGAGCTGTCGGGAAGCAGATTG	1392	Ş
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3 139		1332	δĀ
840	TCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG	781	망
3 133	TCCGCTCTTAACAGCAGTGCCAACCCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG	1272	Ş
3 780	AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG	721	皮
3 1271	AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCCTG	1212	γQ
720	ACAGTGCTGGTCTTCCTCTGTGGCCTTTTGGCATTCAGTGGGCCCTGTTTTTCC	661	망
121:	ACAGIGCIGGICITCCICCICIGIGGCCIGCCITIGGCAITCAGIGGGCCCIGITITCC	1152	Ş
2 660	AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTC	601	Дb
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109	ATCGCGTGGCTGTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGGTC	1032	γQ
540	TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA	481	망
103	TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA	972	Ş
1 480	GTCATGTGTGTCCTGGGCCCTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTC	421	망
971	GTCATGTGTGTGCTGTGGGCCCTGTCCCTGCTGCGAGTATCCTGGAGTGGATGTTC	912	ð
3 420	TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCG	361	В

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	AX498194 Seguence	AR477201 Sequence	E39999 Novel G pro	റ	AF474991 Homo sapi	Novel	Segu	AF474989 Homo sapi	E40003 Novel G pro	AX921831 Sequence			AF474988 Homo sapi	BD103571 Novel G p	AR477199 Sequence	Homo	BD095749 Novel gua	AX923125 Sequence	E43451 Novel prote)6 Sequ	E43450 Novel prote	AX646849 Sequence	AY042216 Homo sapi		Seque	AB065846 Homo sapi

ALIGNMENTS

Qу 181	Db 121	Qу 121	Db da	Ş,	망	β	Query Match Best Local Si Matches 2618;	ORIGIN	source	FEATURES		JOURNAL	TITLE	ALTHORS	neepo exice	ORGANISM	KEYWORDS SOURCE	VERSION	ACCESSION	Locus	RESULT 1 AX429465
11 CAGTCTGTAGAGCTATTAGCCAGTTAAACCCATTTCCTTCATAAATTTCCCAGTCTCAGG 240	11 CACCAGGATTGGAAGCTTCCTGAGGCCTCCCCAGAAGCAGAAGCTGCTATGCTTCTTGTA 180	11 CACCAGGATTGGAAGCTTCCTGAGGCCTCCCCAGAAGCAGAAGCTGCTATGCTTCTTGTA 180	61 CCTCCCTCTCTTACTCCTGCTCTCACCATGTGAGACGCCTCGCTCCCCCTTTGCCTTT 120	61 CCTCCCTCTCTCTACTCCTGCTCTCACCATGTGAGACGCCTCGCCTCCCCCTTTTGCCTTT 120	1 AACAATTGCCGCGAATTCGGCACGAGATGAAATCTAGTTGTTTAAAAGCGTGTAGCACCT 60	1 AACAATTGCCGCGAATTCGGCACGAGATGAAATCTAGTTGTTTAAAAGCGTGTAGCACCT 60	Match 100.0%; Score 2618; DB 6; Length 2618; Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0; es 2618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	12618	Location/Qualifiers	-	encoding human gpcr proteins, and uses thereof Patent: WO 0234914-A 1 02-MAY-2002;	human g-protein coupled recept	Shoo O Reasley R M and Wei M H	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Homo sapiens (human)	AX429465.1 GI:21540763	Sequence 1 from Patent WO0234914.	• •	

1261 CCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCT 1320	1201 CCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTT 1260	1141 CCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTTTGGCATTCAGTGGG 1200	081 TCCTGCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGA 114	21	61 AGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGTGATTCTGTTTGGTGTGAAACGTCAG 10	ACCTGTCATCGGTCATGTGTGTGTGCTGCTGCTGGGGCCCTGTGCTGCTGCGGAGTATCCTGG	GCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCGCGCCCAGAT 9	TCCTCAGTCCTGTGATGACCTTTCCCTACTTATAGGCCTAAGCATGCTGAGGCGCCATCA 84	21 GCGGCCACATTATATGTTCGCCGTTACGCCTCATCATATATCCGCCATCCCAATCTCCAAAA 78 	61 GCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCTCTTCCTTA 72	601 TTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGC 660	41 GACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCG 6	81 GGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACG 54 	21 TGGGATGTCAAACAGGATAAAGAAGAATGGAAAGCAAATCCTCATGGGTCATCAGACTGG 48 	61	ol Arcccaaggigcittccigcigiciicagiciccigciggigiciccagigicicaar 3	181 CAGTCTGTAGAGCTATTAGCCAGTTAAACCCATTTCCTATAAATTTCCCAGTCTCAGG 240 241 TATTTCTTTTTAGCAATTTGAGAATGAACTAATACACAGACAG
2341 TAGTITIN	2281 GTA	2221 AT 2221 AT	2161 2161	Qy 2101 GCCCTTC	Qy 2041 CTGTCAT	Qy 1981 GAGAGAG Db 1981 GAGAGAGA	Qy 1921 GAGTICTO	Qy 1861 TCATGTTC Db 1861 TCATGTTC	Qy 1801 CCTGATAQ Db 1801 CCTGATAC	Qy 1741 ATTGTAA1		1621		Qy 1501 TGCTGCCC Db 1501 TGCTGCCC	Qy 1441 GAAGCAG Db 1441 GAAGCAG	1381 1381	Oy 1321 CCTTTAGG
TITTATGGCTGTTTACATGAGAAGCAAAACTGAAAACATCTGACCTTTCCATGACAA 2400		TINAAGIIGAAAITAICITGAAAACCAITAITAITAICACTIACAATICITTCAGIT 2280 		GCCCCTTCCCCTTGAGAACTGGTAACTTCTTATTTAGCTCTTCCTGGACTAATGAACTAG 2160		GAGAGAGATTCTCCCTTCATAAAAACAGTCTTAGAAATTGGTTTTATGAATAGCCCTCTC 2040 	TTCTGCTACCTCTAAATTCCATTGAATTCTCAGATATAAAGCAAAATAATGACCTTA 1980 	TCATGTTCCCTTTATGACTGGAGGCATTACTGCAGTTGGAAGCTCAATTCTTAATAAGT 1920 			ACATTTTCCCTGTTATCTTGCACTGAATCTTTCTTACTGAACACTTTTTCTGCACTTTTC		TCTCAGTGGTCCCTCAAGGTCTTCGAATAGATGTTTATCTAACCTGACAGTTGCAGTTTT 1620 	TGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCTCAGAAATG 1560	GAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTTGAGAGCAA 1500 		CTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGG 1380

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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Raderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Gollins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Daz, J. S., Dodge, S., Faro, S., Cooke, P., Dearellano, K., Dalagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M., McRean, P., McRernan, K., Meldrin, J., Meneus, L., Mihova, T., McRean, V., Murphy, T., Naylor, J., Matthews, C., McCarthy, M., McRean, V., Murphy, T., Naylor, J., Nells, L., Mihova, T., Meldrin, J., Meneus, L., Mihova, T., Meldrin, J., Meneus, L., Miova, T., Mersa, V., Maymen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M.
B 3 (bases 1 to 91923)

B birren, B., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardya, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyan, S., Gord, S., Craham, L., Grand-Pierre, N., Hagos, B., Karatas, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
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Birren,B., Nusbaum,C. and Lander,B.
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sapiens chromosome 11, clone CTD-3038L12, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (24-JAN-2002) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Yeil, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, I., Zimmer, A. and Zody, M.

Birect Submission

NAL

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 91923)

Gardyns, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Deway, K., Diaz, J.S., Dodge, S., Farra, S., Ferreita, P., FitzGerald, M., Gage, D., Galagan, J., Gardyns, S., Gord, S., Gerham, L., Grand-Pierre, N., Hagos, B., Horton, L., Huhe, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindbad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Marthy, M., Meidrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Macdonald, P., Major, J., Matthews, C., Kmatt, A., Kells, C., Landers, T., Levine, R., Lindbad-Toh, K., Waratas, A., Kells, C., Landers, T., Levine, R., Mishou, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Weil, D., Oliver, J., Peterson, K., Smith, C., Sponcer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Birect Submission
The Stanger, P., 1996, P., P., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Watshington, edu/Rw/RapeatMasker.html
Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Milson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Birect Submission
The Stanger of Center
Center code: MIBR
Web Site, http://www-seq.wimit.edu
Contact: sequence submissionsegenome.wi.mit.edu
Center code: MIBR
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Only the first 91.9 kb of this clone are being submitted. The remainder overlaps accession number AC055860 [WICGR project L9785].

/rpt family="Line" complement (1858. .1917) /rpt family="L2" /rpt_family="iman" complement(2274. .2327) /rpt_family="L2" .ene 4713 /rpt 1671 /rpt_family="L2" 900. . . 1001 comp. Location/Qualifiers Į, 护 clone_lib="CITD2 Human è organism="Homo sapiens" clone="CTD-3038L12" family="L1MD2" _type="genomic DN xref="taxon:9606" _family="L1MD2" family="L2" lement (251. BAC"

8547 GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCA 8488	Db	/rpt_family="MER5A" complement(3265032747)	repeat_region
1422 GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGGAAGGAA	Q	3182231850. /rpt family="(GA)n" - 2020.	
8607 CTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAG 8548	Db	3154ī31821 /rpt_family="AluSx"	- 1
CTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAG 1	Ş	complement (3124731341) complement (3124731341) /rpt_family="MIR"	repeat_region
ATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTT	р ў	/ # PU _ remix y = "PLAE" 31198.	repeat_region
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1242 IGTCATGTGCATCTAGTITCCATTTTCCTGTCCGCTCTTAACAGGAGTGCCAACCCCATC	g .S	/rpt tamily="WSTA" 30412. 30452 /rot family="UTG)"	repeat_region
CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATCGGCAAAGGCCTAGTATTT) B	/rpt_family="AluJo" complement(2933729755)	repeat_region
CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTT	. Q	/rpt family="MIR" complement(2900229304)	
8847 CTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCTCTGTGGCCTG 8788	DЪ	Complement (28194 C. 28287) Complement (28194 C. 28287)	repeat_region
1122 CTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTG 1181	Qy	complement (2749527796) /rpt family="AluSg"	t
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8967 GTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGTT 8908	р ў	/rpc_ramily="Mik" complement(2686327139) /rpc_family="MBR41C"	repeat_region
	? 5	/IDC Lamily="FLAM C" complement()=	repeat_region
	3 5	/ IPC IRITLY = LIMB5	repeat_region
	? 5	/rpt_tam1ly="8VA" 2621926361	
	\$ \$	/rpt_family="(T)n" complement(2463926213)	
AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCCATCTGGTAC) D	/rpt_family="L1PA6" 2461124637	
AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC	. Q	/rpt_family="L1PA4" 2018524476	
CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCCTACTTTATAGGCCTA	Db	/rpt_family="L1PA6" 1959120184	
CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA	Q	/rpt family="L1PB1" 1775219590	
9267 GCCGACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATC 9208	D _D	/rpt_family="L1PB1" complement(15002. 17751)	
702 GCCGACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATC 761	Qy	/rpt_family="LTR33" complement (1461914992)	repeat_region
9327 CTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCG 9268	Db	/rgt_family="MSTA" 1200	
642 CTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCG 701	, QQ	/IDE family="LTR33" /IDE family="LTR33" /IDE family="LTR33"	
9387 ACGGGGTTGACGTTGCCGTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGG 9328	ఠ	1207212409 /rpt_family="MER2"	
582 ACGGGGCTGACGTGCATCGTTTCCCTTTGTCGCGCTGACAGGAAACGCGGTTTGTGCTCTGG 641	Q.	complement(1147911644) /rpt_family="MIR3"	repeat_region
GAACTGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTC 9	D		repeat_region
TOTAL STATEMENT OF THE	\$ 8	/ IDC Lamily="birds" complement(10716 .10825)	repeat_region
462 TCATGGGTCATCAGACTGGGGTTTCTGAGCATTCAACCATTCCAGTCTGGGTACA 521	g. 8	/rpt family="AluSc" complement(71867526)	
	Mat	57965837 /rpt_family="(TAPA)n" 58385875	repeat_region
81.3%	Que	55365795 /rpt_family="Alusc"	

:	2562 TGAACACAGAAAATAAATTAGGAGGATCCTGGTGCTGGAAAAAAAA
2561 7408	02 CCAGACGCCAAACAATATTGTAAGTTCAAATTCTATGAGGTATCCAAATTAGGAAATTCT
2501 7468	STGCTAAGGAAAATAAG
2441 7528	382 TCTGACCTTTCCATGACAATCTCAATTATGGTATCTGGATAATAACTTACAGTTGGTACA
2381 7588	322 TCTGATTGTAACTTTCAGTTAGTTTTATGGCTGTTTACATGAGAAGCAAAACTGAAAACA
2321 7648	2262 CTTACAGATTCTTTCAGTTGTAGGAGAATTCTTCATACTTCCAGGTTTTGTATAAATTGT
2261 7708	2202 ATTGGAAACCTCAATATTGATTTTAAAGTGGAAATTATCTTGAAAACCATTTATTATTCA
2201 7768	2142 TCCTGGACTAATGAACTAGTGAGGAGCCTATAAATATGTCCCACCAGTTTCATTTTGGCC
2141 7828	2082 TCTAGTAAAGACAATCGTGGCCCCTTCCCCCTTGAGAACTGGTAAGTTCTTATTTAGCTCT
2081 7888	
2021 7948	
1961 8008	902 AGCTCAATTCTTAATAAGTGAGTTCTGCTACCTCTAAATTCCATTGAATTCTGAGATATA
1901	AAATCATGTTCCCTTTTATGACTGGAGGCATTACTGCAGTTGGA AAATCATGTTCCCTTCTATGACTGGAGGCATTACTGCAGTTGGA
1841 8128	782 TCTTTATACTTGTTTCCTACCTGATAGTATCAAAAAGGAAGATTCCTTATTAATCTGTCA
1781 8188	722 CACTTTTCTGCACTTTTCATTGTAATAAAAGGAGTTGCTGTCCACAAACCCCTAAAACTCT
1721 8248	662 TCTCCTTGATATTACCAATACATTTTCCCTGTTATCTTGCACTGAATCTTTCCTACTGAA
1661 8308	602 ACCTGACAGTTGCAGTTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGAT
1601 8368	
1541 8428	1482 GACAGGACTTTGAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTA

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                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-FBB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (CB 3 (bases 1 to 172939)

RS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Ngyyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct, Shbmission
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Submitted (05-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 172939)

Birren, B., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
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Submitted (01-OCT-2002) Whitehead Institute/MIT Center for Genome
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Score 2128.6; Pred. No. 0; 0; Mismatches

DB 9; 14;

Length 172939;

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complement(17827. 17000)
/rpt family="LME3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (16587. .16598)

/note="<30 qual SNGL region"

complement (16607. 16612)

/note="<30 qual SNGL region"

complement (16746. .17360)
                                                                                                                                                                                                                                                                                             19933. .19941
/note="<30 qual SNGL region"
20320. .20609
                                                                                                                                                                               /note="<30 qual SNGL region" complement (21118. .21398)
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complement(11344..11683)
/rpt_family="L2"
                                                                                                                                                                                                                                                                    complement (20684.
/note="<30 qual SNGL region"
           note="probably T; possibly C"
21160. .21167
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20879. .20883
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                                                       note="<30 qual SNGL region"
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                                                                  note="probably A; possibly G"
1153. .21158
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                                                                                                           e="probably A; possibly G"
                                                                                                                                                       family="AluSx"
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. .2077
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1542 GCCTTCTGCCTCAGAAATGTCTCAGTGGTCCCTCAAGGTCTTCGAATAGATGTTTATCTA 1601	S82 ACCORDET CALCUTE CANCELLE CONTROLLE CONT
RESULT 4 AC020568 LOCUS LOCUS AC020568 LOCUS DEFINITION Homo sapiens chromosome 20 clone RP11-206C1, WORKING DRAFT SEQUENCE, 24 unordered pieces. ACCESSION AC020568 4 GI:9280789 VERSION AC020568 4 GI:9280789 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT. SOURCE Homo sapiens (human)	Db 112802 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; 938
Sequencing vector: plasmid; 78
Sequencing vector: plasmid; 78
Chemistry: Dye-primer ET; 93% of reads
Chemistry: Dye-terminator Big Dye; 7% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179082 bases at least Q40
Consensus quality: 183120 bases at least Q30
Consensus quality: 183448 bases at least Q20
Toport 5:00.000.0000
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Submitted (04-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 205000; agarose-fp
Insert size: 190318; sum-of-contigs
Quality coverage: 3.99 in Q20 bases; agarose-fp
Quality coverage: 4.34 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: H_NH0206C01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 192618)
Waterston, R.H.
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1 (bases 1 to 192618)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown
contig of 2670
gap of unknown
contig of 3068
gap of unknown
contig of 3588
gap of unknown
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124286
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                                           /note="assembly_name:Contig41"
153983. .169994
                                                                             /note="assembly_name:Contig40"
138709. .153882
                                                                                                                                             /note="assembly_name:Contig38"
109341. .124285
                                                                                                                                                                                92244. .109240
                                                                                                                                                                                                                                                 /note="assembly_name:Contig35"
67189. .77656
                                                                                                                                                                                                                                                                                                                /note="assembly_name:Contig33"
49853. .57604
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
            /note="assembly_name:Contig42"
170095. .192618
                                                                                                              /note="assembly_name:Contig39"
124386 ..138608
                                                                                                                                                                                                                                                                                                                                                     42574. .49752
                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig26"
                                                                                                                                                                                           /note="assembly_name:Contig37"
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/note="assembly_name:Contig29"
24716. .28301
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|7977. .21534
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12039. .14708
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gap of unknown length
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contig of 16012 bp in
gap of unknown length
contig of 22524 bp in
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of unknown length
ig of 16997 bp in length
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of 14945 bp in
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	1297 Db 158239 157218 Qy 2378	1178 CCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTT 1237	1119 CCGCTGACCAGGCT-GTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCGTGGG 1177 Db 158119 157041 CCGCTGAGGATGTTCGAGGGTGATCATCCTCCTCATGGTGGTGGTTGTTCCTCCGCGGGTGT 157100	Qy 2138	1002 GTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGTT 1061	942 CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGAŤTCT 1001 Qy 2018	882 CACTGCCGCCCCAGATACCTGTCATCGGTCATGTGTGTCTCTGGGCCCTGTCC 941	Qy 1898 TGGAAGCTCAATTCTTAA Qy 822 AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCGTGCCATCCTGTGGCCCATCTGGTAC 881	821 Qy 1838 821 Db 157759	QY 702 GCCGACTTCCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATC 761 761	1718 157639	157579	157519	157459	157399	157339
8 9		& & &	9 8	1138 CTCTTCCTGGACTAATGAACTAGTGAGGAGCCTATAAATATGTCCCACCAGTTTCATTTT	078 GGTTTCTAGTAAAGACAATCGTGGCCCCTTCCCCCTTGAGAACTGGTAAGTTCTTATTTAG 	:018 TTGGTTTTATGAATAGCCCTCTCCTGTCATTTGTCCACAGCATGGTGACATGTTGGCCTT	958 TATAAAGCAAAATAATGACCTTAGAGAGAGATTCTCCCTTCATAAAAACAGTCTTAGAAA 	.898 TGAARCTCAATTCTTAATAAGTGAGTTCTGCTACCTCTAAATTCCCATTGAATTCTCAGA 	9 8	ω ω	9 8	ν α	, 60	ο ο α	φα	9

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Sirren, B., Linton, L., Nusbaum, C., Lander, B., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K., Liu, G., MacDean, C., Macdonald, P., Major, J., Marquis, N., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Meldrim, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Pocca, P., Poman, T., Rosetti, M., Roy, A., Santte, R., Schauer, S.
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                                                                                                                Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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1 (bases 1 to 156839)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-81D23
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AC107948
Submitted (26-JUN-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                          Submission
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11, clone RP11-81D23, complete sequence.
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L24483
Center clone name: 81_D_23
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/clone_lib="RPCI-11 Human Male BAC"
complement(1...80)
    /rpt_family="L2"
7738. .7826
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/rpt_family="MIR"
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7387. 7502
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complement(2791. .3)
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/db_xref="taxon:9606"
/chromosome="11"
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family="Alusx"
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	TGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGG 585	Qy 526 TGACAC
	GGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAAC 525	Qy 466 GGGTCA Db 156085 GGGGCA
	70.4%; Score 1842.8; DB 9; Length 156839; 92.2%; Pred. No. 0; vative 0; Mismatches 157; Indels 10; Gaps 4;	Query Match Best Local Similarity Matches 1987;' Conser
	complement(2210522314)	repeat_region
1426 CCCTGGAGCTGGGAAAGCAGATTGGAGCAGTAAGGAAGAACTTCTGCCCTCTCA 1481		
	Complement (20478 20761) Db Complement (20478 20790) Db Complement (20478 20790) Db Complement (20478 20790) Complement (20478 20790) Complement (20478	repeat_region
1366 AGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAA 1425	Complement (1981419962) /rpt family="FRAM" Oy	
1306 ACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCC 1365	/rpt_family="MER81" Qy complement(1930319604) /rpt_family="AluJb" Db	repeat_region
155305 ATGTTTATCTGGTTTGCATGTCCTGTCCTCTAAACAGTAGTGCCAACCCCATCATTT 155246	/IDE family="AluSx" Db Complement (1800318119)	repeat_region
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155365 TCGCCATTCTGGGGGCCCTAATTTACAGGATGCACCTGAATTTGGAAGTCTTATATTGTC 155306	/ Apt_ramily="Alusc"	repeat_region
25		repeat_region
26 CCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCT		
155485 GTGTTTCCAGCCTGGTCCTGCTCAGGATCCTCTGTGGATCCCGGAAGATGCCGCTGA 155426	complement (1463514757) /rpt_family="LTR23"	repeat_region

1006 GGTGTGAAAGGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTT	/rpt family="LTR48" (27	repeat_region
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TGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTTAGTGGTGGTGATTCTGTTT 1005		repeat_region
155665 GCCGCCCCCACACACACTGTCAGCGGTCGTGTGTGTGTCCTGCTCTGGGGCCTGTCCCTGC 155606	/ TPC	
25 TGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCTGTTCTGTGGCCCATCTGGTACCGCT	9" 13348)	
826 TGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACT 885	/rpt_family="LTR56"	repeat_region
ATCTCATCCGCAAAATCCTCGTTTCTGTGATGACCTTTCCCTACTTTACAGGCCTGAGTA	[ement(1211712389) _family="Alur"	
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706 ACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGCCGTTAGCGCCTCATCAATATCCGCC 765	/rpc_family="LTR56"	repeat_region
155905 TGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGCCGCAGCAG 155846		repeat_region repeat region
46 TGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGGCCG	810067 _family="(TG)n"	repeat_region
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25 TGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGG	273)	repeat_region

RESULT 6 AC023078/c LOCUS AC023078 AC023078 AC023078 AC023078 AC023078 AC023078 VERSION AC023078 AC023078 GI:20198710 KEYWORDS HTG.	2322 154228 2382 154168 2442 154108 2502 154048 2559 153988	2022 154525 2082 154466 2142 154406 2202 154346 2202 154346 2202	Qy 1662 TCTCCTTGATATTACCAATACATTTTCQ
8 bp DNA linear´ PRI 23-APR-2002 clone RP11-583F24, complete sequence.	UT		TCTCCTTGATATTACCAATACATTTCCCTGTTATCTTGCACTGAATCTTTCCTACTGAA 1721
	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	SOURCE ORGANISM REFERENCE AUTHORS TITLE TOURNAL REFERENCE AUTHORS
Landers, T., Lehoczky, J., Levine, R., Lindblad-Ton, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, G., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,	Oliver, J., Peterson, K., Phunkhang, P., Pèrre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauber, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Submitted (19-APR-2002) Whitehead Institute/MIT Center for Genome Submitted (19-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 163718) Birren, B., Linton, L., Nusbaum, C., Lander, B., Ali, A., Allen, N., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreita, P., Fithugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lancque, K., Lamazares, R., Tahocar, T., Tarora, P., Tarora, P., Lancares, R., Tarora, R., Lancares, R., Lancares, R., Lancares, R., Tarora, J., Lancares, R., Lancares, R., Lancares, R., Tarora, J., Lancares, R., Lancares, R., Lancares, R., Tarora, J., Lancares, R., Lancares, R., Lancares, R., Tarora, R., Lancares, R., Lancares, R., Lancares, R., Tarora	Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. Direct Submission Submitted (08-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Dases 1 to 163718) Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barria, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cock, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Galagan, J., Karatas, A., Kells, C., LaRcoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Micova, T., Mienga, V., Murphy, T., Naylor, J., Maneus, L., Mihova, T., Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bilaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 163718) E 1 (bases 1 to 163718) Birren,B., Linton,L., Nusbaum,C., and Lander,E., Abraham,H., Allen,N., Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horron,L., Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K., McPheeters,R., Meldrim,J., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Ollvar,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Traviers, M., Trivis, N., Trijilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L6254
Center clone name: 583_F_24
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4460. .4927
                                                                                                                                                                                                        complement (12553. .12696)
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14277. .14341
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/db_xref="taxon:9606"
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                     GCCGACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGCCGGTTACGCCTCATCAATATC
                                                                                                                                                             ACGGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGG
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                                                                CTCCTGGGCTGCCGCATGCGCAAGGAACGCCTTCTCCATCTACATCCTCAACTTGGCCGCA 71328
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REFERENCE AUTHORS TITLE JOURNAL	1782 TCTTTATACTTGTTTCCTACCTGATAGTATCAAAAAGGAAGATTCCTTATTAATCTGTCA 1841 	
REFERENCE AUTHORS TITLE	1722 CACTTTTTCTGCACTTTTCATTGTAATAAAAGGAGTTGGTGTCCACAACCCTAAAACTCT 1781	
SOURCE	1662 TCTCCTTGATATTACCAATACATTTTCCCTGTTATCTTGCACTGAATCTTTCCTACTGAA 1721	
ACCESSION VERSION	1602 ACCTGACAGTTGCAGTTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGAT 1661	
RESULT 7 AC139482/c LOCUS DEFINITION	1542 GCCTTCTGCCTCAGAAATGTCTCAGTGGTCCCTCAAGGTCTTCGAATAGATGTTTATCTA 1601	
Φ.	1482 GACAGGACTTTGAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTA 1541	
Db 695 Qy 25		
Qy 25	1422 GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCA 1481	
on.	1362 CTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGTGGCTTCCTCAG 1421	
Db 696	7 ATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGCCAAAATAGGCAGAACCTGAAGCTGGTT	
Оу 23	0707 IGAGAGATTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTAGAGATTOTAAAATAGAGAGAG	
Db 697	1242 ISTRATIGICATORAGITICCATITICCIGICOGCICTIAACAGCAGIGCCAACCCCATC 1301 10187 TGTCATGTTCATTTTTTTTTTTTTTTTTTTTTTTTTTTT	
Оу 23	/ CCCTTTGGCATTCAGTTTTTCCTATTTTATGGATCCACGTGGACAGGAGAGTCTTATTT	
Db 697	CCTTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTT	
Оу 22	7 CIGACCAGGCIGIACGIGACCATCCIGCTCACAGTACTGGTCTTCCICCTCTGIGGCCTG	
Db 698	CTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTG	
Оу 22	CTCTGTGGGTCCAGCCTGGTCCTGATCAGGATTCTCTGTGGATCCCGGAAGATACCG	
Db 698	CTCTGTGGGTCCAGCCTGGTCCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCG	
Qy 21	7 GCTTGGTGTCAAACATCAGATTTCATCACAGTCGCGTGGCTGATTTTTTTATGTGTGGTT	
•	GTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGGTT	
Оу 20	71087 CTGCTGCGGAGCATCCTGGAGTGGATGTTATGTGGCTTCCTGTTCAGTGGTGCTGATTCT 71028	
סם 700	942 CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT 1001	
Qy .20	7 CGCTGCCACGCCCCACACCCTGTCAGCGGTGGTGTGTGTCCTGCTCTGGGCCCTGTCC	
סם 700	CACTGCCGCCCCAGATACCTGTCATCGGTCATGTGTGTCTGGGCCCTGTCC 941	
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165490 bp DNA linear HTG 04-FEB-2003 Beguence, 12 unordered pieces.

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ACTIVEFIN. 2 (bases 1 to 165490)
2 Toint Genome Institute.
Direct Submission
Submitted (04-FEB-2003) Production Sequencing Facility, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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DOE Joint Genome Institute.

Sequencing of Human Chromosome 5

Unpublished BOB Joint

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74779 GAACTGACACCAATCAACGGAACTGAGAGACTCTTTGCTACAAGCAGACCTTGAGCCTC 74720 582 ACGGGGCTGACGTGACGCTTCCCTTGTCGCGCTGACAGGAAACGGGGTTGTGCTCTGG 641	GAACTGACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTC	462 TCATGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACA 521	y Match 68.5%; Score 1792.2; DB 2; Length 165490; Local Similarity 91.1%; Pred. No. 0; hes 1949; Conservative 0; Mismatches 183; Indels 7; Gaps 4;	/chromosome="5" /clone="RP11-583F24" /clone_lib="RPCI human BAC library 11"	1165490 /organism="Homo sa /mol_type="genomic /db_xref="taxon:96	114464: contig 114564: gap of 165490: contig	67058: contig 67158: gap of 84928: contig	contig gap of contig	17019: contig of 6053 17019: contig of unknown 17119: gap of unknown 22433: contig of 5314	contig of 2888 gap of unknown contig of 4098	1 1249: contig of 1249 1250 1349: gap of unknown 1350 3680: contig of 2331	* runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will	* NOTE: This is a 'working draft' sequence. It currently * consists of 12 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary (Saga between the Cortigs are represented as	insert size: 175000; agarose-fi insert size: 164390; sum-of-co overage: 3.94 in Q20 bases: sum overage: 4.19 in O20 bases: sum	Summary Statistics Consensus quality: 147035 bases at least Q40 Consensus quality: 155210 bases at least Q30 Consensus quality: 155867 bases at least Q30	Project Information Center Project Name: 1518520 Center clone name: RPCI-11_583F24	Center Code: JGI Web site: http://www.jgi.doe.gov	, 2800 Mitchell Drive, Walnut Creek, CA 94 nter nome Institute
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Homo sapiens chromosome 5 clone RP11-583F24, WORKING
SEQUENCE, 12 unordered pieces.
AC139482
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HTG; HTGS_PHASE1; HTGS_I
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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Length 165490;

GGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAAC 525

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* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence es as soon as it is available and the accession number will be preserved.
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DOE Joint Genome Institute.
Direct Submission
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Center Code: JGI
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1 (bases 1 to 165490)
DOB Joint Genome Institute.
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AGCCHARGECH AACHAIAIIGIANG I CAMAIICIAI GNOSIAI CERNII INCOMMI 	B &	1424 AACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGT 1479
	S & &	1364 CCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGA 1423
CATCTGACCTTTCCATGACAATCTCAATTATGGTATCTGGATAATAACTTACACTTGGTA	B 8	TTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCT
2320 GTTCTGATTGTAACTTTCAGTTAGTTTTATGGCTGTTACATGAGAAGCAAAACTGAAAA 2379	음 <i>성</i>	TCATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCCATCAT
2260 CACTTACAGATTCTTTCAGTTGTAGGAGAATTCTTCATACTTCCAGGTTTTGTATAAATT 2319	음 <i>성</i>	CTTCGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTG
2200 CCATTGGAAACCTCAATATTGATTTTAAAGTGGAAATTATCTTGAAAACCATTTATTATT 2259	B &	
	p Q	1064 CTGTGGGTCCAGCCTGGTCCTGGTCAGAATTCTCTGTGGATCCCGGAAGATGCCGGT 1123
TTTCTAGTAAGACAATCGTGGCCCCTTCCCCTTGAGAACTGGTAAGTTCTTATTTAGCT	D Qy	TIGGIGIGAAACGTCAGATITCATTACAAICGCGIGGCIGGITITITITAIGIGIGGIICI
	B 8	GCTGCGGAGTATCCTGGAGTGGAGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCTGT
1960 TAAAGCAAAATAATGACCTTAGAGAGAGATTCTCCCTTCATAAAAACAGTCTTAGAAATT 2019	용 <i>정</i>	GCCGCCGCCCAGATACCTGTCATCGGTCATGTGTGTGTCCTGTGGGCCCTGTCCCT
1900 GAAGCTCAATTCTTAATAACTGAGTTCTGCTACCTCTAAATTCCATTGAATTCTCAGATA 1959 	B &	826 TGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACT 885
	D QQ	766 ATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTAAGCA 825
CTTCTTTATACTTGTTTCCTACCTGATAGTATCAAAAAGGAAGATTCCTTATTAATCTGT	В QV	ACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGGCGTTACGCCTCATCAATATCCGCC
1720 AACACTTTTCTGCACTTTTCATTGTAATAAAGGAGTTGCTGTCCACAACCCTAAAACT 1779	B &	646 TGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCCGGCCG
	B 8	586 GGCTGACGTGCATCGTTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCC 645
TATACTICACA I CANALITATICA CACAGAAAGCATTAGTCTGACAATGTTTAG) B &	526 TGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGG 585
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1002 GITTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTATGTGTGTG	882 CACTGCCGCCGCAGATACCTGTCATCGGTCATGTGTGTCCTGCTCTGGGCCCTGTCC 941	762 CGCCATCCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA 821 [642 CTCCTGGGCTGCCGCATGCGCAGGAACGCTGCTCCACCTACATCCTACATCCTCACCTGGTCGCG 701 [22 GAACTGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAACGAGACCCTGACCTTC	/ Match 56.7%; Score 1483.8; DB 6; Length 2040; Local Similarity 91.4%; Pred. No. 0; nes 1596; Conservative 0; Mismatches 147; Indels 4; Gaps 2; 462 TCATGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACA 521	PATENT: WO 2004042402-A 1 21-MAY-2004; Bayer HealthCare AG (DE) 10		CQ815414 Sequence 1 fr CQ815414 CQ815414.1 G
B & B & B &	\$ B Q B	OV B V B 1	S S B	0 0 0 0 0 0 0 0 0	S B S B #	5	, p & p &	YQ dd
1917 TCTAGTARAGACAACTGTGGCCCCTTCCCCTTGAGAACTTTAAGTGCTTATTTAGCTCT 1976 2142 TCCTGGACTAATGAACTAGTGAGGAGCCCTATAAATATGTCCCACCAGTTTCATTTTGGCC 2201	GAGCAAAATAATGTCCTTAGAGACAGACTCTCCTCATAAAAACACTCTCACCTATTGG TTTTATGAATAGCCCTCTCCTGTCATTTGTCCACAGCATGGTGACATGTTGGCCTTGGTT	1677 GACTATGTTCCCCTGAAAATCATGTCCCTTCTATAAAAAAAA	1558 CACTTTTCTTGCAAATTTTCTTGATAAAAAGGAAAGTTCCTGACAAAACCCTAAAAAACCCTAAAAACAC- 1616 1782 TCTTTATACTTGTTTCCTGATAGTATAAAAGGAAAGGAA	1438 ACCTGACAGTTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTAGAT 1497 1662 TCTCCTTGATATTACCAATACATTTTCCCTGTTATCTTGCACTGAATCTTTCCTACTGAA 1721 1498 TCTCCTTGATATTACCAACACATTTTCCCTGTTATCTTCCACTGAATCTTTCCTACAGAA 1557 1498 TCTCCTTGATATTACCAACACATTTTCCCTGTTATCTCACACTGAATCTTTCCTACAGAA 1557 1722 CACTTTTTCTGCACTTTTCATTGTAATAAAAGGAGTTGCTGCTCACAACCCTAAAACTCT 1781		1362 CICLAGAGGECIELIGEAGARCAE GELIGARGE GENERALIGANGE INGREGORIA CONTROLLER C		CCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTT

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Mammalia; Eutheria;
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Patent: WO 0183555-A 15 08-NOV-2001;
CALIFORNIA INSTITUTE OF TECHNOLOGY (
Location/Qualifiers
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CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT
                                                                                                                      AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC
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Primates;
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Ş	g Q	Query Best L Matche	ORIGIN			CDS	gene	FEATURES source	TITLE	MEDLINE PUBMED REFERENCE	AUTHORS TITLE	ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 11 AY042213 LOCUS	D C	\$ B &	B 8	
522 GAACTGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTC 581	462 TCATGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACA 521	Query Match 56.7%; Score 1483.8; DB 9; Length 2040; Best Local Similarity 91.4%; Pred. No. 0; Matches 1596; Conservative 0; Mismatches 147; Indels 4; Gaps 2;	CGFUFSGADSAWCQTSDFITWAWLIFLCVUCGSSLVLLIRILGGSRKIFUTRLYVTI LLTVLVFILLCGLPFGIQPFLFLWIHVDREVLFCHVHLVGIFLSALNSSANPIIYFFVG SFRQRQNRQNLKLVLQRALQDASEVDBGGGQLPEBILBLSGSRLEQ"	/db_xref="G1:15546062" /translation="MDPTISTLDTELTDINGTEETLCYKQTLSLTVLTCIVSLVGLTG /kranslation="MDPTISTLTELTDINGTEETLCYKQTLSLTVLTCIVSLVGLTG /ANAVUTMLLGCRMRRNAFSIYILNLAAADPLFLSGRLIYSLLSFISIPHTISKILYPVN MFSYFAGLSFLSAVSTERCLSVLWPIWYRCHRPTHLSAVVCVLLWALSLLRSILEWML	/note="Mas.related gene X1" /codon_start=1 /product="G protein-coupled receptor" /protein id="AAK91804.1"			Loca 1 /org /mol	Direct Submission Direct Submission Submitted (19-JUN-2001) Division of Biology Institute of Technology, 1201 B. California 91125. USA	21435808 11551509 2 (bases 1 to 2040) 2 (bases 1 to 2040)		M Homo sapie Eukaryota; Mammalia;	AY042213.1 GI:15546061	AY042213 AY042213 Ayound sanions G protein-counied	2004 ATTGGAA 2040	TCCTGGA	TCTAGTAAAGACAATCGTGGCCCCTTCCCCCTTGAGAACTGGTAAGTTCTTATTTAGCTCT	
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RESULT 12
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ORGANISM
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RS Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.B.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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Homo sapiens G protein-coupled receptor MRGX3, mRNA
MGC:75450 IMAGE:30383708), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTATGAATAGCCCTCTCCTGTCATTTGTCCACAGCATGGTGACATGTTGGCCTTTGGTT
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(bases 1 to 1697)
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AACGATAAGGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGG AATCCTCATGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGG 516

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Query Match Best Local Similarity

49.7%;

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Conservative

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Score 1300.2; DB 9 Pred. No. 3.9e-309; 0; Mismatches 13;

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Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Li
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mori
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 141 Row: m Column: 20
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 16876452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, R.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                             SFRQRQNRQNLKLVLQRALQDTPEVDEGGGQLPQETLELSGSRLEQ
                            LLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFCHVHLVSIFLSALNSSANPIIYFFVG
                                                                                                                                                                                                                                                                                                                                                                                db_xref="LocusID:117195"
db_xref="MIM:607229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="MGC:75450 IMAGE:30383708"
/clssue_type="Testis"
/clone_lib="NIH_MGC_180"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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TCAGTGGTCCCTCAAGGTC	CAATGCTGCCCTGCCAC	CGGGAAGCAGATTGGAGCAGTGAGG 	AGGACACGCCTGAGGTGGATGAAGG	TGGGCTCCTTTAGGCAGCGTCAAAATAGG 	TTTCCATTTTCCTGTCCGCTCTTAAC	CCCTGTTTTCCAGGATCCA	ytgaccatcctcctcacagtgctggtg 	CTGGTCCTGCTGGTCAGGATTCTCTG:	CAGATTTCATTACAATCG CAGATTTCATTACAATCG	CCTGGAGTGGATGTTCTGTGACTTCCT 	AGATACCTGTCATCGGTCATGTGTGT	ATCAGCACCGAGCGCTGCCTGTCCATC	AAAATCCTCAGTCCTGTGATGACCTTT	CTTAGCGGCCACATTATATGTTCGCC 	SCATGCGCAGGAACGCTGTCTCCATCTA 	GGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGG 	
TTCGAATAGATGTTT TTGACAGTACAATGTT	TTATATGCAT	JAAGAACCTCTGCCC	TIGGAGGGTGGCTTC	GCAGAACCTGAAGC	ACAGCAGTGCCAACC	CCTGGATTGGAAAGTCT CCTGGATTGGAAAGTCT	CTTCCTCCTCTGTG	FTGGATCCCGGAAGA FTGGATCCCGGAAGA	CGTGGCTGGTTTTTTATGTG	CCTGTTTAGTGGTGCTG	rccrgcrcrgggccc	CCTGTGGCCCATCT	TTCCCTACTTTATAG	GTTACGCCTCATCA	CTACATCCTCAACCTGG	CAGGAAACGCGGTTGTGC	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Charna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Chargato, S., Colangel, Y., Colangel, M., Collins, S., Collymore, A., Cook, A., Cheepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamat, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connov, T., O'Donnell, P., O'Neil, D., O'Neil, D., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schupback, R., Stanuer, S., Schupback, R., Stanuen, J., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J. Zembek, L., Zimmer, A. and Zody, M.
Research, 320 Charles Street, Cambridge, MA 02141, USA

23 (bases 1 to 189230)

25 Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkly, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
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Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
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1 (bases 1 to 189230)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 13, 2002 this sequence version replaced gi:20330974. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------ Project Information
Center project name: L21856
Center clone name: 1081_L_13
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                                                                                                  /rpt_family="L2"
4172. .4245
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                                                                                                                                                                                complement (2381.
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198. _223
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                       rpt_family="AT_rich"
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complement(29632. .30526)
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7. 24537)
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[ement(2256)
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_family="L2"
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1475 CCTG	1415 TCCTCAGG 8476 TTCTGAGG	1355 GCTGGTTC 8416 GCTGGTTC	1295 CCCCATCA 8356 CCCCATTA	1235 CTTATTTT .8301TTT	1175 TGGCCTGC 8250 TGACCTGC	1115 GATGCCGC 8190 GATGCCCT	1055 TGTGGTTC	995 TGATTCTG	935 CCTGTCCC 8010 CCTGTCCC	875 CTGGTACC	815 AGGCCTAA	755 CAATATCO	695 GGTCGCGGCCGACTTC	635 GCTCTGGC	577 GCTTCACG	526 TGACACCA 7595 TGACATCA	Matches 1695; Conservation 1695; Conservation 1695; Conservation 1695; Conservation 17535; Conservation 1695; Conservatio
GTCAGACAGGACTTTGAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATG	TCTCAGGAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGC 	CTGGTTCTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGTGGACGCT 	CCCATCATTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAA 	CTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAA 	TGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGT TGACCTGCCCTTTGGCATTCAGTGATTCCTATTTTCTGGATCCACGTGGA	GATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTG	TGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGCTGGTCAGAATTCTCTGTGGATCCCGGAA 	TGATTCTGTTTGGTGTAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATG 	CTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGC 	CTGGTACCACTGCCGCCGCCCAGATACCTGTCATCGGTCATGTGTGTG	AGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCAT	CAATATCCGCCATCCCAACTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTAT	1 O	GCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCT	GCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGT	TGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGA TGACATCAATCAATAGGACCGAGGAGACCCATCTTCAACATTGTGGCATGGAGATCATGA	vative c
rgagagcaatgctv	STCGGGAAGCAGA' STCATGAAGCAGA'	3CAGGACACGCCT(3CAGGACACGCCT(3GGCTCCTTTAGG 3GGCTCCTTTAGG	AGTTTCCATTTTC AGTTTCCATTTTC	regeccrerrr rgarrccrarrr	GTGACCATCCTC	CTGGTCCTGCTG	STCAGATTTCATTI ATCAGATTTCATCI	CTGGAGTGGATG CTGGAATGGATG	CAGATACCTGTCA:	CATCAGCACCGAGO	CAAAATCCTCAGT(TCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCAT	ATGCGCAGGAACO	CGTTGACCTGGT	AGGAGACTCCT AGGAGACCCATCTT	Mismatches 403; CTGAGCATGGATTCAACCA
GCCCTGCCACCCT	TTGGAGCAGTGAG TTGGGGCCATGAG	GAGGTGGATGAAG GAGGTGGAAGAAG	CAGCGTCAAAATA CAGCTTCAAAACA	CTGTCCGCTCTTA CTGTCCACTCTTA	TCCAGGATCCACC 	CTCACAGTGCTGG CTCAGAGTGCTGG	GTCAGGATTCTCT GTCAGGATCCTTT	ACAATCGCGTGGC ACAGTCACATGGC	TTCTGTGACTTCC	TCGGTCATGTGTG 	CGCTGCCTGTCCA ACTGCCTGTCCA	CCTGTGATGACCT	ATTATATGTTCGC 	GCTGTCTCCATCT:	CGCGCTGACAGGA CCAGCTGGCAGGA	TGCTAC	403; Indels ACCATCCCAGTC ACCATCCCAGCC
TGACAATTATATG	GAAGAACCTCTGC GAAGAGCCTCTGC	GTGGAGGGTGGCT GCAGATGGCGGCT	CTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAA 	ACAGCAGTGCCAA ACAGCAGTGCCAA	TGGATTGGAAAGT GGA	TCTTCCTCTCTG	GTGGATCCCGGAA GTGGATCCCGGAA	TGGTTTTTTATG TGATTTTTTATG	TGTTTAGTGGTGC	ererercrecrereec	TCCTGTGGCCCAT	TTCCCTACTTTAT	CGTTACGCCTCAT	ACATCCTCAACCT ACACCCTCAACCT	AACGCGGTTGT AATGCAGTCATTT	TGCTACAAGCAGACCCTGA 	55; Gaps TTGGGTACAGAAC TTGGGTACAGAAC
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ACCESSION
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Best Local Similarity
Matches 1195; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suwa,M., Asai,K., Akiyama,Y. and Aburatani,H.
Guanosine triphosphate-binding protein coupled receptors
Patent: EP 1270724-A 1273 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
(JP); Center for Advanced Science and Technology Incubation, Ltd.
(JP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX647081 1369 bp D
Sequence 1273 from Patent BP1270724.
AX647081 GI:28800068
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                   CACTGCCGCCGCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCTCTTGGGCCCTGTCC
                                                              AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC
                                                                                   AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC
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CACTGCCGCCGCCAGATACCTGTCATCAGTCATGTGTGTCCTGCTCTGGGCCCTGTCC
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/db_xref="GI:28800069"
/tdanalation="MOSTIPULGTELTPINGREETPCYKQTLSETGLTCIVSLVALTG
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SFRQRQNRQNLKLVLQRALQDTPEVDEGGGWLPQETLELSGSRLEQ"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.6%; Score 1192.6; DB 6; 99.7%; Pred. No. 1.2e-282; tive 0; Mismatches 4;
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. 1	ORIGIN
urce S	FEATURE:
ORS Zhao,Q., Beasley,B.M. and Wei,M.H. E Isolated human g-protein coupled receptors, nucleic acid mole encoding human gpcr proteins, and uses thereof NAL Patent: WO 0234914-A 3 02-MAY-2002; DR CORP NY (IS)	AUTHORS TITLE JOURNAL
Homo sa Homo sa Eukarya Mammal	SOURCE
AX429467 Sequence 3 fr AX429467 AX429467.1 G	RESULT 15 AX429467 LOCUS DEFINITION ACCESSION VERSION KEYWORDS
1311 ACCTGACAGTTGCAGTTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGG	Вb
1602 ACCTGACAGTTGCAGTTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTTGGA	Ą
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1131 GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTT TTTTTTTTTT	₹ ₩
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1302 ATTTACTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTT	유 &
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1242 TGTCATGTGCATCTAGTTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCCATC	Ş
891 CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTT	B &
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1122 CTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTG	\$ 5
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942 CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTC	8

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ATTTTCTGTCCGCTCTTAACAGCAGTGCCAACCCCATC 1301 ATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATC 8337	1242 TGTCATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTG	B &
CTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTT 8277	8218 CCCTTTGGCATTCAGTGGGCCCTGTTTTCCAG	В
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CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA 7857	7798 CGCCATCCCATCTCCAAAATCCTCAGTCCTGTV	DЪ
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STTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACA 521	462 TCATGGGTCATCAGACTGGGGTTTCTGAGCATG	S
Score 1104; DB 6; Length 8622; Pred. No. 1.2e-260; ; Mismatches 5; Indels 0; Gaps 0;	tch 42.2%; Score 1104; al Similarity 99.6%; Pred. No. 1. 1107; Conservative 0; Mismatche	Query Mai Best Loca Matches

Search completed: October 29, 2004, 13:55:27 Job time: 10834 secs

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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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11218.763 Million cell updates/sec
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                                                                                                           A protein coupled receptor; GPCR; signal transduction pathway; G protein Alzheimer's disease; Parkinson's disease; diabetes; dwarfism; colour blindness; retinal pigmentosa; asthma; depression; schizophrenia; sleeplessness; hypertension; anxiety; stress; renal failure; cardiovascular disorder; neural disorder; oncology disorder;
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                                                                                                                                                                                                                                                                                                                                                 This invention relates to novel G protein coupled receptors (GPCRs) and CC their encoding nucleotide sequences. Many medically significant biological processes are mediated by proteins participating in signal transduction pathways involving G proteins. GPCRs are one of the largest receptor superfamilies known. These receptors are biologically important and malfunction of these receptors results in diseases such as Parkinson's, diabetes, dwarfism, colour blindness, retinal pigmentosa and asthma. They are also involved in depression, schizophrenia, sleeplessness, hypertension, anxiety, stress, renal CC schizophrenia, sleeplessness, hypertension, anxiety, stress, renal CC fallure and other cardiovascular, neural, oncology and immune disorders. A modulator of the GPCRs of the invention may have neuroprotective activity whilst the sequences of the invention may be useful for gene CC activity. The invention may also be useful for manufacturing a medicament for preventing, treating or ameliorating a medical condition. The present CC sequence is the DNA sequence encoding a human GPCR of the invention.
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Query Match
Best Local Similarity
Matches 1596; Conserv
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Best Local Similarity
Matches 1596; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to an isolated mas-related gene D (MrgD) polypeptide. The MrgD polypeptides are useful as therapeutics or for identifying compounds, i.e. agonists or antagonists, that alter pain perception in a mammal. The compounds are useful for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain, promoting wound healing, restoring normal sensitivity following injury, or treating ocular conditions, particularly those associated with pressure such as glaucoma. The Mrg genes or proteins may be used as molecular probes for the detection of cells or tissues related to or involved with sensory perception. The present sequence represents a MrgA (Mrg subfamily) encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mas-related gene D polypeptides, useful as therapeutics or identifying agonists or antagonists that alter pain perception mammal for treating impaired sensory perception, e.g. chronic pain or neuropathic pain.
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                                                                                                                                                      Screening for therapeutic agents, useful for treating e.g., urological disorders, comprises contacting a test compound with a Mas-related genux1 polypeptide and detecting binding of the test compound to the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peripheral nervous system disorder; central nervous system disorder; inflammation; respiratory disease; urological disorder; cancer; Mas-related gene XI; MrgXI; G protein-coupled receptor; antianaemic; cytostatic; haemostatic; cardiovascular; cardiant; vasotropic; cytostatic; antiarteriosclerotic; CNS; antiparkinsonian; nootrop neuroprotective; antiarterive; antiinflammatory; antiallergic; thyromimetic; immunosuppressive; antiasthmatic; respiratory;
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                                                                                           Disclosure; SEQ ID NO 1; 124pp; English.
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CC cardiovascular disease, disorders of the peripheral and central nervous CC cancer in a mammal. The method comprises contacting a test compound with CC Mas-related gene XI (MrgXI) polypeptide and detecting binding of the test Compound to GPR3 polypeptide, or determining MrgXI polypeptide activity CC at a certain test compound concentration (or in the absence of the test compound) and at a different concentration (or in the absence of the test compound) and at a different concentration of the test compound or at the CC presence of a compound known to be a MrgXI polypeptide regulator. Also CC described: (1) diagnosing a disease defined above in a mammal; (2) a CC pharmaceutical composition for the treatment of the disease above CC described: (1) diagnosing a disease of mrgXI polypeptide, or a therapeutic CC agent which binds to a MrgXI polypeptide or which regulates the MrgXI CC agent which binds to a MrgXI polypeptide or which regulates the MrgXI CC appleptide activity such as a small molecule, an ARNA molecule, an CC appleptide diseases. MrgXI has antianemic, cytostatic, haemostatic, CC cardiovascular, cardiant, vasotropic, antiarrhythmic, CC cardiovascular, cardiant, vasotropic, antiarrhythmic, cc cardiovascular, cardiant, vasotropic, antiarrhythmic, cc cardiovascular, antiathmatic, respiratory and nephrotropic fine compuspressive, antiathmatic, respiratory and nephrotropic fine composition of MrgXI are therapy. The regulators of MrgXI are useful for preparation of MrgXI activity in a mammal 1. They are also useful for the regulation of MrgXI activity in a mammal. They are also useful for the regulation of MrgXI activity in a mammal having the disease. The molecular biology techniques that have not yet been developed. Cm and for diagnostic purposes. The present sequence encodes human MrgXI is and for teleptor (GCRE).
G protein-coupled receptor (GPCR).
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Sequence 2040 BP; 455 ? 517 C; 457 G; 611 T; 0 ₽; 0 Other;

56.7%; 91.4%;

Score 1483.8;

DB 12;

Length

2040;

문 문 S 문 S 문 S 문 S 문 á 문 S 닭 Ş Query Match Best Local S Matches 1596 Local Similarity hes 1596; Conserv 478 358 658 762 538 702 642 418 298 CGCCATCCCAAAAAAAAATCCTCAGTCCTGTGATGACCTTTTCCCCTACTTTATAGGCCTA 821 GCAGACTTCCTCTCCTCAGCGGCCGCCTTATATATTCCCTGTTAAGCTTCATCAGTATC GCCGACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATC CTCCTGGGCTGCCGCATGCGCAGGAACGCCTTCTCCATCTACATCCTCAACTTGGCCGCA GAACTGACAATCAACGGAACTGAGGAGACTCTTTGCTACAAGCAGACCTTGAGCCTC GAACTGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTC CGCTGCCACCCCCACACACCTGTCAGCGGTGGTGTGTGTCCTGCTCTGGGCCCCTGTCC CACTGCCGCCCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCTCTGGGCCCTGTCC AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCCATCTGGTAC CTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCG ACGGTGCTGACGTGCATCGTTTCCCTTGTCGGGCTGACAGGAAACGCAGTTGTGCTCTGG ACGGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGGTTGTGCTCTGG CCCCATACCATCTCTAAAATCCTCTATCCTGTGATGATGTTTTCCTACTTTGCAGGCCTG Conservative 0 Pred. No. 0;); Mismatches 147; Indels 4 Gaps 537 941 701 717 761 477 417

The present invention describes a method of screening for therapeutic agents useful in treating disease such as haematological disease,

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                                                   Query Match
Best Local Similarity
Matches 1195; Conserv
                                                                                                                                      The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                               New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                      Suwa
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                                                                                                    Sequence 1369 BP;
                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1273; 28pp; English.
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DB; ADC86821.
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CENT ADVANCED SCI & TECHNOLOGY INCUBATIO
                   TCATGGGTCATCAGACTGGGGTTTTCTGAGCATGGATTCAACCATCCCAGTCTTTGGGTACA
     TCCAGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACA
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The present invention relates to a new G-protein coupled receptor (GPCR) peptide. The invention is useful for identifying a modulator of GPCR and for treating a disease or condition mediated by a human protease. The invention is also useful as models for the development of human therapeutic agents, and as guery sequence to perform a search against sequence databases to, for e.g., identify other family members of related sequences. The vector of the invention is useful for producing a GPCR protein or peptide, for conducting cell-based assays involving the GPCR protein or peptide, for or identifying GPCR protein mutants whose functions are affected, and to produce non-human transgenic animals. The present nucleic acid sequence represents the human G-protein coupled receptor (GPCR) gene located on chromosome 3. This sequence encodes the human G-protein coupled receptor (GPCR) protein of the Claim 4; Fig 3; 75pp; English

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                                                                                            ATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTT
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                                               Query Match
Best Local Similarity
Matches 1096; Conserv
                                                                                                                          The invention relates to Mrg (mas-related gene) protein, which is a G-
protein coupled receptor and drg-12 protein, which is a receptor. The
invention is useful for identifying compounds that bind to it, especially
agonists or antagonists. Administration of an agent (e.g. the identified
agonist) that increases the expression of Mrg in a mammal may be used for
treating impaired sensory perception in a mammal, especially pain. The
antagonist may also be useful for treating impaired sensory perception in
a mammal. The present sequence is human MrgX3 DNA
                                                                                                 Sequence 1400 BP; 276 A; 375 C; 363 G; 386 T; 0 U;
                                                                                                                                                                                                                                                                 Isolated polypeptide, Mrg, which is a G-protein coupled receptor isolated polypeptide, drg-12, which is also a receptor, useful for identifying agonists or antagonists for treating pain.
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01-AUG-2000; 2000US-0223344P.
03-NOV-2000; 2000US-00704707.
19-APR-2001; 2001US-0285493P.
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receptor; sensory perception; pain; analgesic; MrgX3; gene;
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NO:673

Homo sapiens.

08-AUG-2002

19-DEC-2001; 2001WO-US050107

LIFESPAN BIOSCIENCES

19-DEC-2000; 2000US-0257144P

<u>අ</u> Roush CL, Brown JP;

P-PSDB; 2003-046718/04.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

Disclosure; Fig 1; 523pp; English

The present invention describes antigenic peptides (1) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an CC antibody against a particular GPCR, and in the production of specific CC antibodies. The peptides and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CPCRs and antibodies are useful for diagnosing and designing drugs for CC treating immune-related diseases, growth-related diseases, cell CC diseases, or autoimmune diseases, growth-related cell proliferative CC diseases, or autoimmune disease, growth-related cell proliferative CC diseases, bacterial, fungal, protozoan or viral infections, costeoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute CC inflammation, allergies, Crohn's disease, diabetes, graft versus host CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, peptides, pain, psoriasis, cancer, pain, psoriasis,

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Sequence 1400 BP; 276 A; 375 C; 363 G; 386 Η. 0 ς; 0 Other;

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Matches 1096; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to an isolated mas-related gene D (MrgD) polypeptide. The MrgD polypeptides are useful as therapeutics or for identifying compounds, i.e. agonists or antagonists, that alter pain perception in a mammal. The compounds are useful for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain, promoting wound healing, restoring normal sensitivity following injury, or treating ocular conditions, particularly those associated with pressure such as glaucoma. The Mrg genes or proteins may be used as molecular probes for the detection of cells or tissues related to or involved with sensory perception. The present sequence represents a MrgA (Mrg subfamily) encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mas-related gene D polypeptides, useful as therapeutics or in identifying agonists or antagonists that alter pain perception in a mammal for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain.
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sensory perception; glaucoma; Mrg; ds.
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1400 BP; 276 A; 375
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                      GCCTTCTGCCTCAGAAATG 1560
                                                                             GACAGGACTTTGAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTA
                                                                                                                                                        GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCA
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Best Local Similarity
Matches 1100; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of t guanosine triphosphate-binding protein coupled receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1369 BP; 276 A; 364 C; 337 G; 392 T; 0 U; 0 Other;
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AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCCATCTGGTAC
                                                              CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCCTACTTTATAGGCCTA 821
                                                                                                                             GCCGACTTCCTCTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATATC
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                                              CCCCATACCATCTCTAAAATCCTCTATCCTGTGATGATGTTTTCCTACTTTGCAGGCCTG
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Location/Qualifiers
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/*tag= a
                                                                     d gene; G-protein coupled receptor; drg-12
perception; pain; analgesic; MrgX4; gene;
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                                                            TGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCTGTTCTGTGGCCCCATCTGGTACCGCT
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The invention relates to Mrg (mas-related gene) protein, which is a G-protein coupled receptor and drg-12 protein, which is a receptor. The invention is useful for identifying compounds that bind to it, especially agonists or antagonists. Administration of an agent (e.g. the identified agonist) that increases the expression of Mrg in a mammal may be used for treating impaired sensory perception in a mammal, especially pain. The antagonist may also be useful for treating impaired sensory perception in a mammal. The present sequence is human MrgX4 DNA
                                                                                                                                                                                                                                                                     Isolated polypeptide, Mrg, which is a G-protein coupled receptor and isolated polypeptide, drg-12, which is also a receptor, useful for identifying agonists or antagonists for treating pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAY-2000; 2000US-020207P.
01-AUG-2000; 2000US-0222344P.
03-NOV-2000; 2000US-00704707.
19-APR-2001; 2001US-0285493P.
                                                                                                                                                                                                                                                                                                                                        WPI; 2002-171346/22.
P-PSDB; AAE21297.
                                                               Sequence 1604 BP; 337 A; 420 C; 399 G; 448 T; 0 U; 0 Other;
                                                                                                                                                                                                                                         Disclosure; Page 130-132; 185pp; English.
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              similarity 91.0%;
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Score 1013.6; DB 6
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                                                                                                                                                          G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; garaft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MrgX4 G protein-coupled receptor nucleotide SEQ
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GGCTGACGTGCATCGTTTCCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCC

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765 646 705 586 TGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGG

TGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAATCAGACCCTGAGCTTCACGG

GGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAAC 525

GGGGCACCAGACTAGAGTTTCTGAGCATGGATCCAACCGTCCCAGTCTTCGGTACAAAAC

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407 466 Matches 1090; Query Match Best Local Similarity

Conservative

<u>,</u>

Mismatches 104;

Indels

4.

Gaps

Length 1604;

38.7%;

Score 1013.6; DB 8; Pred. No. 4.5e-273;

Sequence 1604 BP; 337 A; 420 C; 399 G; 448 T; 0 U; 0 Other;

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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP3519) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting the CR antibodies. The peptides and antibodies for GPCRs are useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for CPCRs and antibodies are useful for diagnosing and designing drugs for CR GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, call corresponding GPCRs. The antigenic peptides for CR diseases, or autoimmune diseases, growth-related diseases, call corresponding and designing drugs for cost atherosclerosis, bacterial, fungal, protozoan or viral infections, cost atherosclerosis, bacterial, fungal, protozoan or viral infections, can atherosclerosis, bacterial, fungal, protozoan or viral infections, can atherosclerosis, bacterial, fungal, protozoan or viral infections, can atherosclerosis, bacterial, fungal, protozoan or viral infections, cost disease, parkinson's disease, multiple sclerosis, paraft versus host cost disease, parkinson's disease, multiple sclerosis, paraft versus host cost protosoan, can atherosclerosis, cancer, cardiomyopathy, chronic and acute cost parafty, depression, schizophrenia, dementia, mental retardation, memory cost parafty, and sease, and immunociasoays and immunociasoays, abacteria, cancer, cardiomyopathy, parafty versus host cost parafty, parafty par
New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.
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MAS-1
mas-related gene D; MrgD; Analgesic; Vulnerary; Ophthalmological;
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New mas-related gene D polypeptides, useful as therapeutics or in identifying agonists or antagonists that alter pain perception in a mammal for treating impaired sensory perception, e.g. chronic intractable
                                                                                                               Disclosure; SEQ ID NO 32; 220pp; English
                                                                                                                               pain or neuropathic pain.
                                                                                                                                                                                                                                26-JUN-2002; 2002US-00183116
                                                                                                                                                                                                                                                  13-MAY-2003; 2003WO-US015004
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DB; ADH08537.
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The present invention relates to an isolated mas-related gene D (MrgD) polypeptide. The MrgD polypeptides are useful as therapeutics or for identifying compounds, i.e. agonists or antagonists, that alter pain perception in a mammal. The compounds are useful for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain, promoting wound healing, restoring normal sensitivity following injury, or treating ocular conditions, particularly those associated with pressure such as glaucoma. The Mrg genes or proteins may be used as molecular probes for the detection of cells or tissues related to or involved with sensory perception. The present sequence represents a MrgA (Mrg subfamily) encoding sequence.

Sequence 1604 BP; 337 A; 420 C; 399 G; 448 T; 0 U; 0 Other;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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GTGGGTCCAGCCTGGTCCTGCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCGCTGA 1125
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                                                                                           GGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCT 1065
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ilarity 91.0%;
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1254	1195 GACGGGACTTTGAGAGCAACACTGTCCTGCCACCCTTGACAATTACATGCGTTTTTCTTA
1541	1482 GACAGGACTTTGAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTA
1194	1135 GCCTGGAGCTGTCGGGAAGCAGATTGGGGCCATGAGGGAGAGCCTCTGCCCTGTCAGTCA
1481	1426 CCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCA
1134	1075 AGAGGGCTCTGCAGGACAAGCCTGAGGTGGATAAAGGTGAAGGGCAGCTTCCTGAGGAAA
1425	1366 АСАСССТСТССАССАСАСССТСАССТСАССТВАССТВАС
1074	1015 ACTICTICGIGGGCTCCTITAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCC
1365	1306 ACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCC
1014	955 ATGITTATCTGGTTTGCATGTCCCTGTCCTCTAAACAGTAGTGCCAACCCCATCATTT
1305	1246 ATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCCAACCCCATCATTT
954	895 TCGGCATTCTGGGGGCCCTAATTTACAGGATGCACCTGAATTTGGAAGTCTTATATTGTC
1245	1186 TIGGCATTCAGIGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTC
894	835 CCAGGCTGTACGTGACCATCCTGCTCACAGTGCTGGTCTTCCTTC
1185	1126 CCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCT
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Search completed: October 29, 2004, 10:54:55 Job time : 1234 secs 유 정 유

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586.8

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12049.920 Million cell updates/sec
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CN831931
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CN840024
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11.1	11.1	11.2	11.3	11.3	11.4	11.4	11.5	11.5	11.5	11.6	11.7		11.8	11.8	11.8	11.9	12.1	12.2	12.4	12.8
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ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION source Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. B 1 (bases 1 to 889) B 1 (MagC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (199) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Kristi A. Egland, Ira Pastan CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be Homo sapiens (human) CA455045 CA455045.1 GI:24905369 High quality sequence stop: Location/Qualifiers found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM14285 row: h column: 07 EST AGENCOURT_10735784 MAPcL Homo CA455045 mRNA sequence. /lab_host="EMDH10B" /clone lib="MAPCL" /clone lib="MAPCL" /clone lib="MAPCL" /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Egland, James J. Vincent, Robert Strausberg, Kristi A. Egland, James J. Discovery of new breast Bungkook Lee & Ira Pastan: Discovery of new breast /clone="IMAGE:6722551" /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCAP" organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" .889 gd 688 743. bp mRNA linear EST 12-NOV-2002 sapiens cDNA clone IMAGE:6722551 5',

Manuscript submitted."

cancer genes encoding

membrane and secreted proteins.

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KEYWORDS
SOURCE
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 863)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectionpublished (1999)
                                                                                                                                                                863 bp mRNA linear ES
AGENCOURT 15864324 NIH MGC_145 Homo sapiens cDNA clone
IMAGE:30706618 3', mRNA sequence.
CN835944
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CN835944.1 GI:47941599
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3.9e-174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard, Ph
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
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                            CCTCTGTGGCCTGTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTG 1228
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30706618"
/tissue_type="mixed"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib=WIH MGC 145"
/clone lib=WIH MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORPs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EccRV-XmmI/XhoI-3', 5'-EccRV-XmmI/NotI-3', EccRV (TA cloned, non-directional).
For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.lnnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
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AGENCOURT 15658848 NIH MGC 145 Homo
IMAGE:307766619 5', mRNA sequence.
CN843633
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: GPCR Consortium CLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://imagge.llnl.gov
Plate: IRBI4 row: e column: 12
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Tissue Procurement: GPCR Consortium
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1 (Dases 1 to 835)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-ECORV-XmnI/XhoI-3',
5'-ECORV-XmnI/NotI-3', ECORV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.lin1.gov/image/rearrayed_plates/IRBI.preSV.dat
a Note: this is a NIH_MGC Library."
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Query Match

23.1%;

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AUTHORS
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 764)

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, B., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
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Tel: 216 431 9900
Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Scott
CTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGTC
                                                                                                                           TGCTGGTCTTCCTCCTCTGTGGCCCTGTTGGCATTCAGTGGGCCCTGTTTTCCAGGA 1215
                                                                                                                                                                                            TTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTCACAG 1155
                                                                                                                                                                                                                                                      CGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGGTCAGGA 1099
                                                                                                                                                                                                                                                                                               GCTTCCTGTTCAGTGGTGATTCTGCTTGGTGTCAAACATCAGATTTCATCACAGTCG
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/clone lib="Achersys RAGE Library"
/clone lib="Achersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/ibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/db_xref="taxon:9606"
/cell_line="HT1080"
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Pred. No. 1.1e-146;
0; Mismatches 76;
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Matches 695; Conser
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Bldg: 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
(LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: IRB14 row: e column: 10
High quality sequence stop: 653.
Location/Qualifiers
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1 (bases 1 to 827)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
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                            CAGTCCTGTGATGACC-TTTCCCTACTTTATAGGCCTAAGCATGCTGAGCACCATCAGCA
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CGTTTCTGTGATGACCTTTTCCCTACTTTACAGGCCTGAGTATGCTGAGCGCCATCAGCA
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/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30706617"
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/lab_host="DH108"
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Pred. No. 2.3e-146;
0; Mismatches 88;
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Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.B. Cc
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 924)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTC
                                                                                                                                       ACGTGACCATCCTCACAGTGCTGGTCTTCCTCTCTGTGGCCTGCCCTTTTGGCATTC
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        TGCAGGACAAGCCTGAGGTGGATAAAGGTGAAGGGCAGCTTCCTGAGGAAAGCCCTGGAGC
                         TGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCCTGGAGC
                                                                    TGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTC
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/clone lib="NIH MGC_145"
/note="vector: pcDNA3.1; Site_1: varies by clone; Site_2:
varies by clone; ORFs were PCR-amplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmmI/XhoI-3',
5'-EcoRV-XmmI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.lln1.gov/image/rearrayed_plates/IRBI.preSV.dat
a Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo Bapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30706614"
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Pred. No. 4.8e-145;
0; Mismatches 78;
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TITLE
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Best Local Similarity 98.1%;
Matches 657; Conservative
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Duke Eye Center, Erwin Rd, Box
Tel: 919 681 4085
Fax: 919 684 8983
Email: pedro.gonzalez@duke.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gonzalez,P., Epstein,D.L. and Borras,T.
Characterization of gene expression in human trabecular
using single-pass sequencing of 1060 clones
Invest. Ophthalmol. Vis. Sci. (2000) In press
Contact: Pedro Gonzalez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTM1-025F1 HTM1 Homo sapiens
BE439409
BE439409.1 GI:9438891
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                   ATATCCGCCATCCCAAAAATCCTCAGTCCTGTGATGACCTTTCCCCTACTTTATAG
                                                                                                                     TCGCGGCCGACTTCCTTTCCTTAGCGGCCACATTATATGTTCGCCGCTTACGCCTCATCA
                                                                                                                                                                                                                            GCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGC
                                                                                                                                                                                                                                                                                 GTACAGAACTGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGA
                           GCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCT
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/db_xref="taxon:9606"
/tissue_type="Trabecular meshwork"
/clone_Tib="HTM1"
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Pred. No. 4.3e-142;
D; Mismatches 7;
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Matches 621; Conserva
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                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Zegnang Han
Chinese Nactional Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, |
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 662)

1 (bases 1 to 662)
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AV731610 HTF Homo sapies
AV731610
AV731610.1 GI:10849155
                                                                                                                                                                                                                                                                                                                                                                                 Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
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TCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGATTCTCCTTGATATTACCAA
                                                                   GTCTCAGTGGTCCCTCAAGGTCTTCGAATAGATGTTTATCTAACCTGACAGTTGCAGTTT
                                                GTCTTAGTGGTAACTCAAGGTCTTCAAATAAATGTTTATCTAACCTGACAGTTGCAGTTT
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                                                                                                                Conservative
                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
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/clone="HTPAKDOB"
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/dev_stage="Adult"
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                                                                                                                                                                                                   /clone_lib="HTF"
/note="Vector: pl
Xhol"
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95.5%;
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Pred. No. 9.3e-136;
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REFERENCE
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BG208126/c
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Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                         Homo eapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                    Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
                                                                                                                                                                                           Contact: Scott
Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        787 bj
RSJ27616 Athersys RAGE Library
BG208126
BG208126.1 GI:13729813
                                                                                                                                                                           3201 Carnegie Ave,
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1 (bases 1 to 787)
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                                                                                     quality sequence stop: 1
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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RESULT 10 CN843258/c LOCUS

DEFINITION

CN843258 825 bp AGENCOURT 15669738 NIH MGC 145 L IMAGE:30706610 5', mRNA sequence CN843258 CN843258.1 GI:47948913

sequence.

Homo

mkNA linear EST 02-JUN-2004 sapiens cDNA clone

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1407

GGGTGGCTTCCTCAGGAAACCCTGGAG 1433

TGGTGGTATCCTCAGGAAACCCTGGAG

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32

1347

AACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGA

1406

93

AGTGCCAACCCCATCATTTACTTCTTCATGGGTTTCGTTAGGCAGCATCAAAATTAGCAG

92

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ACCESSION VERSION

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Query Match
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Matches 649
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                                                                                                                                                                        CTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGAT
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AGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAAATAGGCAG 1346
                                                          TGGGAAGTCTTATATTCTCATGTTCATCTGCCTTCCATTTTCCTGGCGTCTCTTAACAGC
                                                                                                                                           CTCCTCTGCGGCCTGCCCATTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACATGGAC 213
                                                                                                                                                                                                                                                                                                                     TITTATTTGTGGTCCTCTGTGTGCCCAGCCTGGTCCTAGTGGTCAGGATCCTCTGTGGA
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/note="See 'Creation of Genome-wide Protein Expression
/Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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Pred. No. 5.8e-132;
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Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 825)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov
Plate: IRBI4 row: e column: 03
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                                                                                                                                                                                                                                                            TACCACTGCCGC-CGCCCCAGATACCTGTCATCGGTCATGTGTGTGTCCTGCTCTGGGCCCT
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GCCGCTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGG 1177
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                                                                                                                        TTCTGTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGT
                                                                                                                                                                          GTCCCTGCTGCAGCATCCTGGAATGGATGTTATGTGGCTTCCTGTTCAGTGGTGCTGA
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/lab_host="DH1B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="NIH_MGC_145"
//note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NhoI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous fip site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
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Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 871)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 701.
Location/Qualifiers
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/clone lib="NIH MGC 145"
/clone lib="NIH MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
/aries by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmmI/XhoI-3', 5'-EcoRV-XmmI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30706609"
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/lab_host="DH10B"
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1 (bases 1 to 953)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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AGENCOURT 15864292 NIH MGC 145 Homo
IMAGE: 30706616 3', mRNA sequence.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
                                                Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
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plate: IRBI4 row: e column: 09
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/clone lib="NIH MGC_145"
/clone lib="NIH MGC_145"
/clone lib="NIH MGC_145"
/clone "Yector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:30706616"
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Pred. No. 1.6e-120;
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                                                                                                                                                                                                                                                          CGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCCCCAGATACCT
GCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCAT
                                                                                CATTACAATCGCGTGGCTTGTTTTTTATGTGTGGGTTCTCTGTGGGGTCCAGCCTGGTCCT
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216 361 9596
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Location/Qualifiers
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/mol_type="mRN,"
/db xref="taxon:9666"
/cell_line="HT1080"
/clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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Pred. No. 9.3e-116;
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CD051096 CD051096.1 GI:30488660
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDKM39 row: e column: 24
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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High quality sequence start: 3
High quality sequence stop: 741.
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Tissue Procurement: Dr. Jamie Thompson, University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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AGAAAAAGATAAGGGGTCACCAGACTAGGGTTTCTGAGCATGGATCCAACCATCTCAACC
                            AGCAAATCCTCATGGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTC
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                                                                                         Conservative
                                                                                                                                                                                                  /clone_lib="NIH_MGC_173"
/note="Vector: pDONR201;
LIBR_PRIMING - oligo dT;
LIBR_PROVIDER - Bradfield
                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                              tissue_type="embryonic trophoblasts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                         18.5%;
87.5%;
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                                                                                    Score 483.4; DB 6;
Pred. No. 5.8e-115;
0; Mismatches 76;
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                                                                                                                                                     Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
         CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBI4 row: e column: 04
High quality sequence stop: 464.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="vector: pcDNA3.1; Site_1: varies by clone; oRFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortum. Cloning sites vary by pcDNA3.1 by the GPCR Consortum. Cloning sites vary by pcDNA3.1 by the GPCR Consortum. Cloning sites vary by pcDNA3.1 by the GPCR Consortum. Cloning sites vary by pcDNA3.1 by the GPCR Consortum. Cloning sites vary by pcDNA3.1 by the following: 5'-EcoRV-xmnI/XhoI-3', 5'-EcoRV-xmnI/XhoI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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Search completed: October 29, 2004, 16:07:28 Job time: 7925 secs

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Result
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ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1 AX429465 LOCUS DEFINITION ACCESSION VERSION SOURCE ORGANISM ORIGIN FEATURES KEYWORDS Query Match 100.0%; Score 2618; Best Local Similarity 100.0%; Pred. No. 0; JOURNAL source Zhao,Q., Beasley,E.M. and Wei,M.H. Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpcr proteins, and uses thereof Patent: WO 0234914-A 1 02-MAY-2002; PE CORP NY (US) 2618 bp Sequence 1 from Patent W00234914. Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. AX429465.1 GI:21540763 Location/Qualifiers /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" DNA 뮵 6; Length 2618; linear PAT 21-JUN-2002

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Submitted (24 JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

B (bases 1 to 91923)

B irren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Forceira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, L., Halme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Yeil,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Birect Submission

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Submitted (24 AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 91923)

Barna,N., Bastlen,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Cook,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Cook,A., Cook,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Petralira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Karatas,A., Kells,C., Landers,T., Levine,R., Jinchald-Toh,K., McCatthy,M., Meddrim,J., Meneus,L., Grand-Pierre,N., Hagos,B., Chomen,L., Hune,M., Iliey,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Dewar,M., Orogno,L., Hune,M., Tliey,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Mupphy,T., Naylor,J., Mardham,J., Grand-Pierre,N., Hagos,B., Mupphy,T., Naylor,J., Mardham,L., Grand-Pierre,N., Hagos,B., Shuhar,J., Cook,P., Pierre,N., Raymond,C., Retta,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Will,D., Oliver,J., Peterson,K., Fersion, P., Pierre,N., Schuber,J., Schubback,R., Schuber,J., Schubback,R., Schuber,J., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

B Direct Submissione Street, Cambridge, MA 02141, USA
On Sep 3, 2002 this sequence version replaced gi:22474954.

The Canter ode: Wilk
Web Site: http://www-seq.wi.mit.edu
Contact: sequence submissione@genome.wi.mit.edu
Contact: sequence submissionesgenome.wi.mit.edu
Contact: sequence submissionesgenome.wi.mit.edu
Contact: sequence submissionesgenome.wi.mit.edu
Contact: sequence submissionesgenome.wi.mit.edu
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Only the first 91.9 kb of this clone are being submitted. The remainder overlaps accession number AC055860 [WICGR project L9785].

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complement(251.
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                                                                                                                                                                                             clone_lib="CITD2 Human BAC"
                                                                                                                                                                                                       clone="CTD-3038L12"
                                                                                                                                                                                                                  map="11"
                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                 _family="L1MD2"
                                                                                                                                                                                                                                       xref="taxon:9606"
                                                                                                                        _family="L1MD2"
                                                       Tement (1858. .1917)
_family="L2"
                                  family="THE18"
                                                                              family="L1MD3"
                        .2327)
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1426	3182231850 /rpt_family="(GA)n"	repeat_region
8603 AGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAA	3154131821 /rpt family="AluSx"	repeat_region
1366 AGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAA	complement (3124731341) /rpt family="MIR"	repeat_region
ACTICITICGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCC	/ pc _ remity=	repeat_region
1306 BOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTTOTT	lement (31075.	repeat_region
8723 ATGTCCATTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTT	/*pt family="(TG)"	repeat_region
1246 ATGTGCATCTAGTTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTT	complement(2933729755)	repeat_region
TRACE A TRACE A CONTROL TO THE TRACE A	/ EDC	repeat_region
1184 THE TRANSPORT OF T	complement (28194. 28287)	repeat_region
1120	/rpc_ramily="Alusg" complement(27797. 28030) /rpt_family="MARBAIC"	repeat_region
1176 - 7757 - 775	ш.	repeat_region
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	26719)	repeat_region
	N.SI	repeat_region
946 TECGGACTATCCTGGAGTGGATCTTCTGTGACTTCCTGTTTAGTGGTGGTGATTCTGTTT	/ PDC - POWER - PDC - PD	repeat_region
9083 GCCGCCCAGATACCTCTCATCGTCATGTGTGTCTCTGGGCCCTGTCCTGC	complement (24639) .26213) /ref family="SVA" .26213)	repeat_region
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826 TGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACT	1959120184 /rnt family="".1PA4"	repeat_region
9203 ATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCCTACTTTATAGGCCTAAGCA	1752 .19590 /rpt family="L1PA6"	repeat_region
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9263 ACTTCCTTTACCGCCCACATTATATGTTCGCCGTTACGCCTCATCAATATCCGCC	complement(1461914992) /rpt family="L1PB1"	repeat_region
706 ACTICCTCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATCCGCC	13295. 13552 /rpt family=rrr33"	repeat_region
CONSTRUCTION AND THE PROPERTY OF THE PROPERTY	complement (12876 13294)	repeat_region
646 TOPPOTATOPORATOPORTATOPORTATOPOTATOPORTA	=	repeat_region
9383 GGCTGACGTGTTTCCCTTGTCGCGCTGACAGGAAAACGCGGTTGTGGCTCTGGCTCC	. 12409 amilv="MER2"	repeat_region
586 GGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGGTTGTGCTCTGGCTCC	.11644)	repeat_region
Db 9443 TGACACCAATCAACGGACGTGAGGAGACCCCTTGCAAGCAGAACCCTTCACGG 9384	/*Dt family="Vir" /rpt family="VI" /rpt family="VI"	repeat_region
DDJADJEJDJADJADJEJDADADIKACAGAGAJEJDJEJDAJADADADADAJATATEGGGATOKACHIKACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	amily="Limb4" ment(10716. 10825)	repeat_region
	tamily="AluSc" Lament (71867526)	repeat_region
MATCHES 2130; CONSERVATIVE U; MISMACCHES O; INCELS U; GADS	n"	repeat_region
atch 69.9%; score 1830; DB 9; Length 91923; Similarity 99.7%; Pred. No. 0;	family=", .5837	
	55365795	repeat_region

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	446 TCTGATACATGCTGTGACATACATGAACCTGGAAATA	
	386 ACCTTTCCATGACAATCTCAATTATGGTATCTGGATAAT. 	
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	266 CAGATTCTTTCAGTTGTAGGA	
	206 GAAACCTCAATATTGATTTTA 	
	2146 GGACTAATGAACTAGTGAGGAGCCTATAAATATGTCCCACCAGTTTCATTTTGGCCATTG 2205	
	086 GTAAAGACAATCGTGGCCCCT	
	026 ATGAATAGCCCTCTCCTGTCATTTG	
	66 AAAATAATGACCTTAGAGAGAGA	
	906 CAATTCTTAATAAGTGAGTTCTV	
	846 ATGTTCCCCTGAAAATCATGT	
. •	786 TATACTTGTTTCCTACCTGATAGTATCAAAAAGGAAGATTCCTTATTAATCTGTCAGACT 18 	
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	666 303	
	606 GACAGTTGCAGTTTTCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGATTCTC 1 	
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REFERENCE AUTHORS

Submitted (05-SEP-2002) whitehead Institute/MIT Center for Genom Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 172939)

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,

for Genome

JOURNAL TITLE

Zembek,L., Zimmer, Direct Submission

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밁 7403 CACAGAAAATAAATTAGGAGGATCCTGGTGCTGGAA 7368

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REFERENCE
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SOURCE
ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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AL Submitted (14-FBB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (Charles 1 to 172929)

Birren, B., Nusbaum, C., Lander, B., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Chagara, B., Choepel, Y., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand, Pierre, N., Hagos, B., Horton, L., Hhlme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Minga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Daxrellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Daxrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Graham, L., Ubnson, R., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sutrauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Mammalla; Eutheria; Primates; Catar
1 (bases 1 to 172939)
Birren,B., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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COMMENT TITLE JOURNAL

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Direct Submission

Submitted (01-OCT-2002) Whitehead Institute/MIT Center for Genome Man 02141. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L12764
Center clone name: L13_D_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="L1M4"
complement(1395. .1513)
                               /rpt_family="MLT2B1" complement (9265. .106
                                                                                                                  complement (7175. .73
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complement(4009. .4170)
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                                                                                                       complement (8308.
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clone_lib="RPCI-11 Human
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db_xref="taxon:9606"
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                                                                                                                                                                                                                                              family="MER5B"
- .4647
                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="FLAM_A"
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family="Charliel"
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complement(21118..21398)
/rpt_family="AluSx"
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/note="<30 qual SNGL region"
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1153. .21158
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RESULT 4 ACC20568 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE	B & 8	\$ \$ \$ \$, B & B	S B 8	? B &	B 8	B 8	B &	B 성	B 8	B 6	B &	g 4g	문
7 4 568 AC020568 AC020568 ACOZO568 ACOZ	111998 ACGCCAMACAALA IGIAAGIICCAMITICLA IGAGGIAICCAMAILAGAAALIA II 1999 2566 CACAGAAAATTAGGAGGATCCTGGTGCTGGAA 2601 	2946 CLISALACA GELIGIAN CALIGRAM LA LA LIGITA DE LA CONTROLLA DEL CONTROLLA DELA	ATTGIAACTITCAGTTAGTTTATGGTATTAACATGAGAAGCAAAACTGAAAACTA	CAGATTCTTTCAGTTGTAGGAGAATTCTTCATACATCAGAAAACTGTATCTG ATTGTAACTTTCAGTTTATGGCTGTTTTACATGAGAAGCAAAACTGAAAACATCTG ATTGTAACTTTCAGTTTATGGCTGTTTTACATGAGAAGCAAAACTGAAAACATCTG ATTGTAACTTTCAGTTTATGGCTGTTTTACATGAGAAGCAAAACTGAAAACCATCTG	2206 GARACCTCARTATTGARTTTRAKGTGGARARTTATTGARAACCATTTATTATTATTCACTTA 2265 2206 GARACCTCARTATTGARTTTRAKGTGGARARTTATTGARTAKATCACTTA 2265 112258 GARACCTCARTATTGATTTTARAGTGGARATTATCTTGARARACCATTTATTATTCACTTA 112199 2266 CACATTTTTTACTTTCACTTACGAGARTTCTTCCATACTTTCTTGTATARATTGTTTCTTG 2125	GGACTAATGAACTAGTGAGGAGCCTATAAATATGTCCCACCAGTTTCATTTGGCCATTG	GTAAAGACAATCGTGGCCCCTTCCCCTTGAGAACTGGTAAGTTCTTATTTAGCTCTTCCT 		1966 AAAATAATGACCTTAGAGAGAGATTCTCCCTTCATAAAACAGTCTTAGAAATTGGTTTT 2025 	CAATTCTTAATAAGTGAGTTCTGCTACTCTAAATTCCATTGAATTCTCAGATATAAAGC	ATGITCCCCTGAAAATCATGITCCCTTTTATGACTGGAGGCATTACTGCAGTTGGAAGCT	1786 TATACTTGTTTCCTACCTGATAGTATCAAAAAGGAAGATTCCTTATTAATCTGTCAGACT 1845	1/20 1111CHCHCHILLCHARIANANGANGINGCUGCACAACCCTAAAACTCTTCTT 112679 112738 TTTTCTGCACTTTTCATTGTAATAAAAGGAGTTGCTGCCACAACCCTAAAACTCTTCTT 112679	

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JOURNAL REFERENCE
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Waterston,R.H.
Direct Submission
Submitted (04-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jul 19, 2000 this sequence version replaced gi:9211362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Phrap; version 0.990319
Consensus quality: 179082 bases at least Q40
Consensus quality: 183120 bases at least Q30
Consensus quality: 185448 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; 93% Sequencing vector: M13; 93% Sequencing vector: plasmid; 7% Chemistry: Dye-primer ET; 93% of reads Chemistry: Dye-primer ET; 93% of reads Chemistry: Dye-terminator Big Dye; 7% of reads
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Mammalla; Eutheria; Primates;
1 (bases 1 to 192618)
Waterston,R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 3.99 in Q20 bases; agarose-fp Quality coverage: 4.34 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 205000; agarose-fp
Insert size: 190318; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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124386. .138608
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Isolated human g-protein coupled receptors, nucleic encoding human gpcr proteins, and uses thereof Patent: WO 0.234914-A 3 02-MAY-2002;
PE CORP NY (US)
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Sequence 3 from Patent WO0234914.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 ACTICCICTICCTIAGCGCCACATIATATGTICGCCGTTACGCCTCATCAATATCCGCC
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                                                      TGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGGCCG
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/mol_type="unassigned DNJ
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1 (bases 1 to 1697)
                                                                                                                                                     BC067292 1697 bp mRNA linear Homo sapiens G protein-coupled receptor MRGX3, mRNA MGC:75450 IMAGE:30383708), complete cds.
                                                                                                                       BC067292
BC067292.1 GI:45501076
                                                                      Homo sapiens
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altechul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Mooze, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rhibin, G.M., Hong, L., Schaefer, C.F., Bhat, N.K., Schaefer, C.F., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rhibin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carrinci, P., M., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hullyk, S.W., Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, J., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., L., Carrinci, E.J., Mortiques, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shovchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., M., Schnerch, A., Schin, J.E., Jones, S.J., and Marra, M.A., Green, E.D., Mortiquez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDMA sequences

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22 (bases 1 to 1697)
22 (bases 1 to 1697)
23 (transberg, R. Direct Submission
34 (22-MAR-2004) National Institutes of Health, Mammalian Submitted (12-MAR-2004) National Institutes of Health, Mammalian Submitted (12-MAR-2004) National Institutes of Health, Mammalian Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, UNIA Library Preparation: Invitrogen Corp COMP Contest: MGC help desk Email: (1949beremille) Natural Health, M.G. E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Canada info@bbcgc. bc.ca

Steve Jones, Barah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Fernather, Marcy L
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 141 Row: m Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 16876452. Location/Qualifiers

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Guanosine triphosphate-binding protein coupled receptors
Patent: BP 1270724-A 1273 02-JAN-2003;
National Institute of Advanced Industrial Science and Technology
National Institute of Advanced Science and Technology Incubation, Ltd.
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Sequence
AX647081
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                 GGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAAC 525
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1606 GACAGTTGCAGTTTTCCACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGA 1660	1546 TCTGCCTCAGAAATGTCTCAGTGGTCCCTCAAGGTCTTCGAATAGATGTTTATCTAACCT 1605 	1486 GGACTITGAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCT 1545	1426 CCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACA 1485 	1366 AGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTTGGAGGGTTGCCTCCTCAGGAAA 1425	306 ACTTCTTCGTGGGCTCCTTTAGGCAGCGGCAAAATAGGCAGAACCTGAAGCTGGTTCTCC 1	1246 ATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTT 1305	1186 TTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTC 1245	1126 CCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCT 1185	1066 GTGGGTCCAGCCTGGTCCAGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCGCTGA 1125	1006 GGTGTGAAACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGGTTCTCT 1065	946 TGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTT 1005	886 GCCGCCCCAGATACCTGTCATCGGTCATGTGTCCTGCTCTGGGCCCTGTCCCTGC 945	826 TGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACT 885	766 ATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCCTACTTTATAGGCCTAAGCA 825	706 ACTTCCTCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATCCGCC 765	646 TGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCCGGCCG	586 GGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCC 645	
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0183555-A 30 08-NOV-2001;
CALIFORNIA INSTITUTE OF TECHNOLOGY (US)
Location/Qualifiers
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                                                                            CGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCG
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SFRQRQNRQNLKLVLQRALQDTPEVDEGGGWLPQETLELSGSRLEQ"
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Query Match 41.6%; Score 1088; DB 6; Length 1400; Best Local Similarity 100.0%; Pred. No. 0; Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/or /mo /db	JOURNAL PATENT: WO 02061087-A 673 08-AUG-2002; Lifespan Biosciences, Inc. (US) FEATURES Location/Qualifiers source 1 . 1400	AUTHORS	NISM Homo sapiens Eukaryota, Me Mammalia, Eut	AX549388 AX549388.1 GI:25814004	RESULT 9 AX549388 AX549388 10CUS AX549388 10CUS DEFINITION Section 673 from Parent WOD2061087.	1393 CAGAAATG	Db 1333 GAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCT 1392 Qy 1553 CAGAAATG 1560	QY 1493 GAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCT 1552	QY 1433 GCTGTCGGGAAGCAGATTGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTT 1492	1373 IC JOHANGACGCC IGANG JOHANG JOHANG JOHANG JOHANG CC JOHAN LOCAIGANA CCCIGGA 1213 TCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCTGGA	1313 TOTAL CONTROL CON	1233 ICLASTITICATITITC TOTTO TABLE OF THE TOTTO THE TOTT	1033 TCAGTGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCA				953 793
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1493 GAGAGCANIGETGECCETGECACCETTGACANITATISCATITETTAGECTTCTGCCT 1392 1333 GAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCT 1392	GCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTT	1373 TCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCTGGA 1432 	1313 CGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGC 1372 	1253 TCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTT 1312	1193 TCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCA 1252	1133 GTACGTGACCATCCTCCCCACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCAT 1192	1073 CAGCCTGGTCCTGCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCGGTGACCAGGCT 1132	AACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGGTC	AACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGGTC	953 TATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTTGGTGTGA 1012	893 CCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCTGCTGCTGCTGCTGCGGAG 952	833 CGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCG 892	773 CTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCCTACTTTATAGGCCTAAGCATGCTGAG 832	713 CTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATCCGGCCATCCCAT 772	653 CCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCT 712	593 GTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTG 652	533 AATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGAC 592	473 CAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACC 532

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KEYWORDS
SOURCE
ORGANISM
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Dong, X., Han, S.-K., Zylka, M.J., Simon, M.I. and Anderson, D.J.
Direct Submission
Submitted (19-JUN-2001) Division of Biology, 216-76, California
Institute of Technology, 1201 E. California Blvd., Pasadena, CA
91125, USA
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1 (bases 1 to 1400)
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                          E43450.1 GI:18627716
JP 2000166576-A/1.
Homo sapiens (human)
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S Watanabe, T., Terao, S. and Matsui, H.

Novel protein G-coupled receptor protein and DNA thereof

Patent: JP 2090166576-A 1 20-JUN-2000;

TAKEDA CHEM IND LTD

OS Homo sapiens (human)

PN JP 2090166576-A/1

PD 20-JUN-2000

PP 30-SEP-1999 JP 1999278116

PR

TAKUYA WATANABE, SHIZUKO TERAO, HIDEKI MATSUI

PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61F43/00,

PC C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12P21/02, C12P21
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PC
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G12N33/53,G01N33/566,G01N33/577//(C12N1/21,C12R1:19),(C12N5/10, PC
G12R1:91),
PC
G12N5/00,C12R1:19),(C12P21/08,C12R1:91),C12N15/00,A61K37/02,
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Location/Qualifiers
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Jorganism='Homo sapiens (human)'.
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   ATCGCGTGGCTGGTTTTTTTATGTGTGGGTTCTCTGTGGGTCCAGCCTGGTCCTGCTGGTC
                                                                                                             GTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTC
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                                                 TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA
                                                                                             GTCATGTGTGTCCTGGGGCCCTGTCCCTGCGGAGTATCCTGGAGTGGATGTTC
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C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
A61P43/00,
C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,C12P21/08, PC
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 0;
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                                                                                             ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC
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   GTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCTCTTCCTTAGCGGCCACATT
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                                                                                                                                                                                                                                                                                                             /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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E43451.1 GI:18627717
JP 2000166576-A/2.
Homo sapiens (human)
M Homo sapiens (human)
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M Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
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Watanabe, T., Terao, S. and Matsui, H.
Novel protein G-coupled receptor protein and
Novel protein G-coupled receptor protein and
Patent: JP 2000166576-A 2 20-JUN-2000;
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Best Local Similarity
Matches 968; Conserv
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PD 20-JUN-2000

PF 30-SEP-1999 JP 1999278116

PR

TAKUYA WATANABE, SHIZUKO TERAO, HIDEKI MATSUI

PI TAKUYA WATANABE, SHIZUKO TERAO, HIDEKI MATSUI

PC C12N15/99, A61K38/00, A61K39/395, A61K49/395, A61K45/00, A61K48/00,

PC R61P43/00,

PC C07K14/705, C07K16/28, C12N1/21, C12N5/10, C12P21/08, PC

G01N33/15,

PC G1N33/15,

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C12R1:91),

PC C12N5/00, C12R1:19), (C12P21/08, C12R1:91), C12N15/00, A61K37/02,

PC C12N5/00, C12R1:91)

PC C12N5/00, C12R1:91)

PC C12N5/00, C12R1:91)

PT S0UTCE /Organism='Homo Bapiens (human)'.
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                            AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC
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C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,A61K39/395,A61K45/00,A61K39/00,C12N15/10,C12P21/02,C12P21/08, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (C12P21/02, C12R1:19), (C12P21/08, C12R1:91), C12N15/00, A61K37/02
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Query Match 35.0%; Score 916; DB 6; Length 969; Best Local Similarity 99.9%; Pred. No. 0; Matches 966; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Matches 966; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy 492 ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACCAATCAACGGACGTGAGGAG 551	/mol_type="unassigned DNA" //db_xref="taxon:9606" 1. 969 1. 969 /note="unnamed protein product" /codon start=1 /protein id="CAP02233.1" /db_xref="GI:40216229" //db_xref="GI:40216229" /tanslation="MDSTIPLYBTELTPINGREETPCYKQTLSFTGLTCIVSLVALTG_ /translation="MDSTIPLYALTPINGREETPCYKQTLSFTGLTCIVSLVALTG_ /translation="MDSTIPLYALTPINGREETPCYKQTLSFTGLTCIVSLVALTG_ /translation="MDSTIPLYALTPINGREETPCYKQTLSFTGLTCIVSLVALTG_ /translation="MDSTIPLYBTATLYBTALTYKTLSILSFVM_ /translation="MDSTIPLYBTATLYBTATLYBTGLTCIVSLYALTG_ /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTG_ /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTG_ /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTG_ /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGMT /db_xref="GI:40216229" /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGMT /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGLTCIVSLYALTGATLYBTGATLYBTGLTCIVSLYALTGATLYBTGMT /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGTMT /db_xref="GI:40216229" /translation="MDSTIPLYBTGLTCIVSLYALTGATLYBTGTMT /translation="MDSTIPLYBTGTMT" /db_xref="GI:40216229" /translation="MDSTIPLYBTGTMT" /db_xref="GI:40216229" /translation="MDSTIPLYBTGTMT" /fdb_xref="GI:40216229" /translation="MDSTIPLYBTGTMT" /fdb_xref="GI:40216229" /translation="MDSTIPLYBTGTMT" /fdb_xref="GI:40216229" /fdb_xre	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Peri,K.G., Moffett,S. and Abran,D. Methods and compounds for prevention and treatment of elevated intraocular pressure and related conditions JOURNAL PALETINES PATURES THERATECHNOLOGIES INC. (CA) FEATURES Location/Qualifiers 1.969 Organism="Homo sapiens"	Oy 1452 GAGCAGTGA 1460 Db 961 GAGCAGTGA 969 RESULT 14 AX923125 LOCUS AX923125 DEFINITION Sequence 1 from Patent WO03080659. ACCESSION AX923125 VERSION AX923125.1 GI:40216228	1332 Q 841 Q 1392 Q 901 Q	1152 ACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCCTCTCTCT
RESULT 15 AP474987 AP474987 LOCUS DEFINITION Homo sapiens G protein-coupled receptor SNSR1 gene, complete cds. ACCESSION AP474987 VERSION AF474987.2 GI:31747894 KEYMORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens EUKaryyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 969)	Db 781 TÖCĞCTCTTAACAĞCAĞTĞCCAACCCĞATCATTTACTTCĞTĞĞĞCTCCTTTAĞĞĞĞĞ 840 Qy 1332 CGTCAAAATAGGCAGAACCTGAAGCTTGTTCTCCAGAGGCACACGCCTGAG 1391	Oy 1092 AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGCCTTACCTCTCTCT	421 GICATGIGICCTGCTCTGGGCCCTGCTCCTGCGGAGTATCCTGGAGTGGATGTTC 972 TGTGACTTCCTGTTTAGTGGTGCTGATTCCTGTTTGGTGTGAAACGTCAGATTTCATTACA	Qy 792 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 851	Qy 612 GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCATGCGCAGGAACGCT 671

V	Вb	β	Вb	S	Qy dg	В	Ş.	Db	Ş	В	8	Db	Ą	Db	Q	Query Matc Best Local Matches 9	ORIGIN					,	CDS	mRNA	FEATURES		JOURNAL	REFERENCE AUTHORS	MEDLINE MEDLINE	TITLE	 	AUTHORS
979 TCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACAATCGCGT 1038	428 GTGTCCTGCTCTGGCCTGTCCCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACT 487	919 GTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGAGTATCCTGGAGTGGAGTGTTCTGTGACT 978	368 CCATCCTGTGGCCCATCTGGTACCACTGCCGCCCCCAGATACCTGTCATCGGTCATGT 427	859 CCATCCTGTGGCCCATCTGGTACCACTGCCGCCCGCCCCAGATACCTGTCATCGGTCATGT 918	799 CCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGT 858		739 CGCCGTTACGCCTCATCAATATCCGCCATCCTCCAATCTCCCAAAATCCTCAGTCCTGTGATGA 798	188 TCTACATCCTCAACCTGGTCGCGGCCGACTTCCTCTTCCTTAGCGGCCACATTATATGTT 247	679 TCTACATCCTCAACCTGGTCGCGGCCGACTTCCTTCCTTTAGCGGCCACATTATATGTT 738	128 CAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCA 187	619 CAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCA 678	68 GCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGA 127	559 GCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCCTTGTCGCGCTGA 618	8 CAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAGACTCCTT 67	499 CAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAGACTCCTT 558	Match 30.7%; Score 805; DB 9; Length 969; ocal Similarity 99.8%; Pred. No. 0; s 905; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		CDFLFSGANSWECETSDFITIAMUVFLCVVLCGSSLVLLVKILCGSKKMPJIKLXVTI LLTVLVFLLCGLPFGIQMALFSRIHLDMKVLFCHVHLVSIFLSALNSSANPIIXFFVG SFRORONRONLKLVLORALODTPEVDEGGGWLPOETTLELGGSKLEO"	NAVVLMILGCEMRENAVSIYILMIVAADFLFLSGHIICSFLELINIEHPISKILSFVM TFFYFIGLSMISAISTERCLSILMFIWYHCREPRYLSSVMCVLLWALSILBKILFIVMF	/btvcein in="AMD000/0.2" /db_xref="GI:31747895" /translation="MDDTIDVIGTEITDINGREETPCYKOTLSFTGITCIVSIVALTG	/codon_start=1 /product="G_protein-coupled_receptor_SNSR1" /protein_id="nanegage 7"	"GPCR"	<pre>/product="G protein-coupled receptor SNSR1" 1969</pre>	xon:9606	location/Qualifiers	on Jun 16, 2003 this sequence version replaced gi:19338907.	w	2 (bases 1 to 969) Ahmad, S., Banville, D., Fortin, Y., Lembo, P.M. and O'Donnell, D.	NAC. NEUROBEL. 5 (3), 201-209 (2002). 2185373 11850634	Proenkephalin A gene products activate a new family of sensory neuron-specific GPRs	, Strom, P	Lembo, P.M., Grazzini, E., Groblewski, T., O'Donnell, D., Roy, MO., Zhang, J., Hoffert, C., Cao, J., Schmidt, R., Pelletier, M., Labarre, M.,

1 547 17 547 17 607 17 607 17 607 17 607 17 607 17 607 17 607 17 607 17 607 17 607 17 607	1399 AAGGTGG 1405 908 AAGGTGG 914	1339 ATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATG	1279 TIAACAGCAGIGCCAACCCCATCATTTACTICTTCGIGGGCICCTITAAGCAGCGICAAA	1219 ACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTGTCCGCTC	1159 TGGTCTTCCTCTGTGGGCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCCAGGATCC	1099 TCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTCACAGTGC	1039 GGCTGGTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGGTCAGGATTC	

Search completed: October 29, 2004, 22:34:19 Job time : 10045 secs

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Abz42595 Human G p
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Aaa29811 Human G p
Abt04875 Human G p
Adc30080 Human GPC
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Adf70583 Orphan re
Aaa29812 Human G p
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Aaa70342 Human nov
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Acc44771 Human G p
Adc12765 Human GPC
Abz35127 Human gen
Aaz10068 Human dor
Aaz10067 Human dor
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Abk52823 Genomic D
Adc86820 Human GPC
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ALIGNMENTS

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ID ARSC2
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XX Huma
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P-PSDB; AAU97598.
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31-MAY-2001; 2001US-00867570.
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Novel isolated G-protein coupled receptor peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise

Claim 4; Fig 1;

75pp; English

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Query Match
Best Local Simi
Matches 2618;
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                                                                                                                                         Human; G-protein coupled; receptor; GPCR; human protease; human therapeutic protein; query sequence; search; gene; ds; sequence database; non-human transgenic animal; gene therapy; chromsome 3.
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                                                                                                                                                                                                                                                                                                         The present invention relates to a new G-protein coupled receptor (GPCR) peptide. The invention is useful for identifying a modulator of GPCR and for treating a disease or condition mediated by a human protease. The invention is also useful as models for the development of human therapeutic groteins, as targets for development of human therapeutic agents, and as query sequence to perform a search against sequence databases to, for e.g., identify other family members of related sequences. The vector of the invention is useful for producing a GPCR protein or peptide, for conducting cell-based assays involving the GPCR protein or its fragment, for identifying GPCR protein mutants whose functions are affected, and to produce non-human forprotein coupled receptor (GPCR) gene located on chromosome 3. This sequence encodes the human G-protein coupled receptor (GPCR) protein coupled receptor (GPCR) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated G-protein coupled receptor peptide useful for treating disorder characterized by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise
                                                                                                                                                                                                                                                                    Sequence 8622
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ds; gene; human; GPCR; guanosine triphosphate-binding protein coupled receptor; gene
                                       Human GPCR gene SEQ ID NO:1273.
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                                                                                                           New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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The invention relates to a novel polynucleotide encoding a guanosine triphosphate-binding protein coupled receptor (GPCR). A polynucleotide the invention may have a use in gene therapy. The polynucleotide and polypeptide are useful for preparing a composition for treating a patie in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor. The polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the patient o H

Sequence 1369 BP; 272 A; 372 C; 340 G; 385 T; 0 U; 0 Other;

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                                                                                                                                               Human MrgX3 (mas-related gene)
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The invention relates to Mrg (mas-related gene) protein, which is a G-protein coupled receptor and drg-12 protein, which is a receptor. The invention is useful for identifying compounds that bind to it, especially agonists or antagonists. Administration of an agent (e.g. the identified agonist) that increases the expression of Mrg in a mammal may be used for treating impaired sensory perception in a mammal, especially pain. The antagonist may also be useful for treating impaired sensory perception in a mammal. The present sequence is human MrgX3 DNA
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01-AUG-2000; 2000US-0222344P.
03-NOY-2000; 2000US-00704707.
19-APR-2001; 2001US-0285493P.
                                                                                                                                                                                                                                                                                                                       Sequence 1400 BP; 276 A; 375 C; 363 G; 386 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide, Mrg, which is a G-protein coupled isolated polypeptide, drg-12, which is also a receptor, identifying agonists or antagonists for treating pain.
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   Burmer GC,
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P-PSDB; 2003-046718/04. ABP81750

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure; Fig 1; 523pp; English

The present invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; CC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in Gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and designing drugs for CC regeneration-related diseases, growth-related diseases, cell CC regeneration-related diseases, growth-related diseases, cell CC diseases, or autoimmune diseases, growth-related cell proliferative diseases, or autoimmune diseases, growth-related cell proliferative continuation, allergies, Crohn's disease, diabetes, graft versus host CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, canxiety, depression, schizophrenia, dementia, mental retardation, memory consistency astima, tuberculosis, obesity, nausea, hypertension, cell consistency astima, tuberculosis, obesity, nausea, hypertension, or any other disorder in which GPCRs are involved. The antibodies may be cused in immunoassays and immunodiagnosis. ABAZ4553 to ABZ4269 encode CC GPCR proteins given in ABP81675 to ABP82018, which are used in the

1400 B₽; 276 A; 375 C; 363 G; 386 T; 0 U; 0 Other;

Ş 밁 Ş 밁 Ś 밁 5 片 8 밁 **&** B 8 Query Match Best Local S Matches 1088 Local Similarity 473 893 613 553 373 1088; 773 713 493 653 433 CAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACC CCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCTGCGGAG CGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCG CTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAG CTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCAT CCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCT GTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTG AATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGAC CAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACC CTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAG CTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCAT CCGCATGCGCAGGAACGCTGTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCT GTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTG AATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGAC Conservative 41.6%; 0, Score 1088; Pred. No. 0; Mismatches В 8 <u>.</u> Length 1400; Indels 0; Gaps 372 552 492 672 0

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New mas-related gene D polypeptides, useful as therapeutics or in identifying agonists or antagonists that alter pain perception in a mammal for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain.
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                                                                                                                                                                                                                                                                       2004-083025/08.
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Disclosure; SEQ ID NO 30; 220pp; English.

SXCCCCCCCCCCX SX F F F F F X R R X The present invention relates to an isolated mas-related gene D (MrgD) polypeptide. The MrgD polypeptides are useful as therapeutics or for identifying compounds, i.e. agonists or antagonists, that alter pain perception in a mammal The compounds are useful for treating impaired sensory perception, e.g. chronic intractable pain or neuropathic pain, promoting wound healing, restoring normal sensitivity following injury, or treating ocular conditions, particularly those associated with pressure such as glaucoma. The Mrg genes or proteins may be used as molecular probes for the detection of cells or tissues related to or involved with sensory perception. The present sequence represents a MrgA (Mrg subfamily) encoding sequence.

Sequence 1400 BP; 276 A; 375 C; 363 G; 386 T; 0 U; 0 Other;

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               Human-derived G protein-coupled e.g. in determining ligands and dysfunction of the protein.
                                                           WPI; 2000-303747/26.
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Claim 6; Page 93-94; 97pp; Japanese
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                         protein and encoding nucleic acid, useful treatment of diseases associated with
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                  AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG
                           AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTTCCATTTTCCTG
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The present sequence encodes a human-derived G protein-coupled protein designated hHI77213, which is isolated from the human hippocampus. The G protein-coupled receptor can be used for preventing, treating and diagnosing genetic diseases associated with G protein-coupled protein, and for regulating cellular functions. The protein-coupled protein, and treat disorders associated with G protein-coupled protein gene dysfunction. It can also be used to identify G protein-coupled protein ligands and generating antibodies and antisera against the protein. It is also useful in constructing recombinant receptor protein expression systems, developing receptor-binding assay systems and screening drug candidates, and can be used as a probe in the genetic diagnosis of G protein-coupled protein disorders
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Query Match 37.0%; Score 969; D Best Local Similarity 100.0%; Pred. No. 0; Matches 969; Conservative 0; Mismatches Sequence 969 BP; 171 A; 280 C; 250 G; 268 T; 0 U; 0 Other; 492 ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG GTGATGACCTTTCCCCTACTTTATAGGCCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT GCGCTGACAGGAAACGCGGTTGTGCTCTTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGGCTGACGTGCATCGTTTCCCTTGTC ATCGCGTGGCTGTTTTTTATGTGTGGTTCTCTGTGGGTCCAGCCTGGTCCTGGTC 109: GTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCGGAGTATCCTGGAGTGGATGTTC GTCATGTGTGTCCTGCGCCCTGGGGCCCTGCTGCGGAGTATCCTGGAGTGGATGTTC 971 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCATCTCCAAAATCCTCAGTCCT ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCATCTCCCAAAATCCCTCAGTCCT ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG ACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTTGGCATTCAGTGGGCCCTGTTTTCC ACAGTGCTGGTCTTCCTCTGTGGCCCTGCCCTTTGGCATTCAGTGGGCCCTGTTTTCC 1211 AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC 115 ATCGCGTGGCTGGTTTTTTATGTGTGGGTTCTCTGTGGGTCCAGCCTGGTCCTGCTGGTC TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA 103: TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCG TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCCCCAGATACCTGTCATCG Mismatches DB 3; Length 969; 0, Indels 0; Gaps 600 540 720 671 611 60 660 480 420 360 851 300 791 240 731 180 120 0

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20-FEB-2001; 2001US-0270266P.
20-FEB-2001; 2001US-0270286P.
06-APR-2001; 2001US-0282032P.
06-APR-2001; 2001US-0282356P.
06-APR-2001; 2001US-0282358P.
06-APR-2001; 2001US-0282358P.
14-MAY-2001; 2001US-028235P.
14-MAY-2001; 2001US-0399208P.
                                                                                                                                                                                                                                                                                         27-NOV-2000;
12-DEC-2000;
20-FEB-2001;
20-FEB-2001;
06-APR-2001;
                                                              The present invention provides the protein and coding sequences of several human G-protein coupled receptors (GPCRs). These can be used in the identification of candidate compounds as receptor agonists or inverse agonists having applicability as therapeutic agents. The present sequent is a GPCR coding sequence of the invention
                                                                                                                                       Novel endogenous and non-endogenous versions of G protein-coupled receptor useful for identification of candidate compounds as receptor agonists or antagonists for use as therapeutic agents.
                                                                                                                                                                                                        Chen
                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31; hRUP32; hRUP33; hRUP35; hRUP35; hRUP37; gene; ss.
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CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the trasngenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR gene of the invention; and kits comprising
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders (e.g., Alzheimer's disease,
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders (e.g., autoimmune disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders (e.g.,
CC anaemia or soreoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates sequences at least 90% identical to the GPCR proteins and nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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                                                               TCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 1331
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                                                                                                                                                                                                           The invention relates to a non-human mammal that carries a DNA integrated with a foreign HI77213 or its mutant gene, or a part of it. The non-human animal is particularly a rat. Such gene shows phenotypes of e.g. cataract onset, transient skin rash and proliferation-promoting activity. The foreign HI77213 gene is a gene that encodes a G protein-coupled receptor (GPCR) protein HI77213. The protein, its encoded DNA and constructed transgenic animals are useful for clarifying pathological mechanism, developing therapeutic methods and screening preventives or remedies for related diseases e.g. cataract, cancer, and dermatitis. The present sequence represents a DNA encoding a human HI77213 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method of identifying ligands to an orphan receptor protein which comprises transforming cells with DNA encoding a fusion protein of the orphan receptor with a fluorescent protein, so that the fusion protein is expressed in the cells (or cell membranes isolated from them) and contacting the cells with the potential ligand to be tested. A suitable fluorescent protein for incorporation in the fusion protein is green fluorescent protein (GPP), for example GPP-1, wild-type GPP, GPPuv or Enhanced GPP (EGPP). The method is useful for the identification of ligands binding to an orphan receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transformation of cells with a fusion protein protein with a fluorescent protein useful for to the orphan receptor.
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23-JUL-2002; 2002JP-00213949.
11-OCT-2002; 2002JP-00298237.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1683 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 206; 594pp; Japanese.
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Fujii R,
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The invention relates to a human GPCR (G protein coupled receptor) designated R-14 (ADF29105), nucleic acids encoding it (ADF29104), and R-14 peptide antagonists (ADF29106-ADF29108). The invention also encompasses vectors and host cells comprising R-14 nucleic acids, and methods of screening for R-14 antagonists. The R-14 receptor is expressed in trabecular meshwork tissue, and is associated with a role in ocular outflow. Inhibition of the receptor results in a reduction of basal intracocular pressure, making the R-14 receptor a useful target for screening for ocular hypotensive drugs. The R-14 peptide antagonists are

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                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                          New substantially pure R-14 polypeptide, useful as drug targets for lowering intraocular pressure and for treating condition such as
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Best Local Similarity
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                                               CGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCCTGAG
                                                                                                           AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG
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Pred. No. 0;
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                                                                                                                                                                  Query Match
Best Local Similarity
Matches 965; Conserv
                                                                                                                                                                                                                                                                                                                             The invention relates to a non-human mammal that carries a DNA integrated with a foreign HI7T213 or its mutant gene, or a part of it. The non-human animal is particularly a rat. Such gene shows phenotypes of e.g. cataract onset, transient skin rash and proliferation-promoting activity. The foreign HI7T213 gene is a gene that encodes a G protein-coupled receptor (GPCR) protein HI7T213. The protein, its encoded DNA and constructed transgenic animals are useful for clarifying pathological mechanism, developing therapeutic methods and screening preventives or remedies for related diseases e.g. cataract, cancer, and dermatitis. The present sequence represents a DNA encoding a human HI7T213 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HI7T213 protein, encoded DNA and transgenic animals for clarifying pathological mechanism, developing therapeutic methods and screening preventives or remedies for related diseases e.g. cataract, cancer, dermatitis.
                                                                                                                                                                                                                                                                               Sequence 966 BP; 171 A; 280 C; 248 G; 267 T; 0 U; 0 Other;
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Matches 917; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 969 BP; 172 A; 282 C; 249 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides encoding novel G-protein coupled receptors useful diagnosis, drug screening, clinical trial monitoring and for the treatment of physiological or behavioral disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-JAN-1999;
14-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 52-53; 61pp; English.
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                                                                          ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCATCTCCAAAATCCCTCAGTCCT
                                                                                                                                GTCTCCATCTACATCCTCAACCTGGTCGCCGGCCGACTTCCTTTCCTTTAGCGGCCACATT
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             GTGATGACCTTTCCCCTACTTTATAGGCCCTAAGCATCCTGAGCGCCATCAGCACCGAGCGC
                                    GTGATGACCTTTCCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 851
                                                                                                                 GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT
                                                                                                                                                                                                                      ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC
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1. .969
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                                                                                                                                                                                                                                                                                                                        Score 867; DB 3; Pred. No. 1e-313; 0; Mismatches
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Search completed: October 29, 2004, 19:33:33 Job time: 1232 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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4 US-09-254-227A-6
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4 US-09-495-050A-164
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4 US-09-254-227A-12
4 US-09-254-227A-13
5 US-09-497-855A-32
6 US-09-497-855A-32
7 US-09-497-810B-2
7 US-09-149-476-179
7 US-09-149-476-179
7 US-09-621-976-14560
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US-09-254-227A-6
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Best Local Similarity
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23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23
0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9	0.9
1425	1364	1364	1353	1353	1350	1126	1126	1126	1100	1092	1092	1092	947	761	761	651	651
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US-08-464-148-1	US-09-828-995B-33	US-09-828-995B-31	US-09-653-285-6	US-08-913-014A-6	US-09-149-476-248	US-10-115-123-89	US-10-012-542-89	US-09-461-325-89	US-08-820-051-3	US-10-115-123-86	US-10-012-542-86	US-09-461-325-86	US-09-673-395A-8	US-10-170-097-71	US-09-641-638-71	US-10-170-097-72	US-09-641-638-72
Sequence 1, Appl	Sequence 33, Appl	Sequence 31, A	Sequence 6, Appli	Sequence 6, Appl	Sequence 248,	_	Sequence 89, Appl	-	Sequence 3, Appl	•	Sequence 86, A	Sequence 86, App.	Sequence 8, Appl	Sequence 71, A	Sequence 71, App.	•	•

ALIGNMENTS

; LENGTH: 969 ; TYPE: DNA ; ORGANISM: Homo & US-09-254-227A-6 APPLICANT: Ahmad, Sultan APPLICANT: Banville, Denis APPLICANT: Benville, Denis APPLICANT: Eventin, Yves APPLICANT: Lembo, Paola APPLICANT: O'Donnell, Dajan APPLICANT: O'Donnell, Dajan APPLICANT: Shi-Hsiang, Shen TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat FILE REFERENCE: 81823/268117 CURRENT APPLICATION NUMBER: US/09/254,227A CURRENT FILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 22 SOFTWARE: PatentIn version 3.0 SOFTWARE: Far SEQ ID NO 6 SEQ ID NO 6 Sequence 6, Application US/09254227A Patent No. 6696257 GENERAL INFORMATION: sapiens 21.2%; Score 554; DB 4; 1 Pred. No. 3.9e-232; Length 969; Rat and Human

373	CCAGCCTCCTCTCCATCC	망
864	805 CCTACTTTATAGGCCTAAGCATGCTGAGGGCCATCAGCACCGAGGGCTGCCTGTCCATCC	Ş
313	254 TACGCCTCATCAATATCAGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTC	οь
804		Ş
253	194 TCCTCAACCTGGTCGCGGCCGACTTCCTTTCCTTTAGCGGCCACATTATATGTTCGCCGT 253	DЬ
744	685 TCCTCAACCTGGTCGCGGCCGACTTCCTTTCCTTTAGCGGCCACATTATATGTTTCGCCGT 744	Ş
193	134 ACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACA 193	Д
684	625 ACGCGGTTGTGCTCCTGGGCTGCCGCATGCGCAGGAACGCTGTCTCCATCTACA 684	Ş
133	74 AGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTCGCGCTGACAGGAA 133	DЬ
624	565 AGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCCTTGTCGCGCTGACAGGAA	Ş
73	14 TCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACA 73	gg g
564	505 TCCCAGTCTTGGGTACAGAACTGACACCCAATCAACGGACGTGAGGAGACTCCTTGCTACA	Ş
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SOFTWARE: Patentin vers
SEQ ID NO 4
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 596; Conserv
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GENERAL INFORMATION:
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APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Fortin, Yves
APPLICANT: Fortin, Yves
APPLICANT: Combon, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
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                                                              CTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCCTGTCCATCCTGTG
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                  GCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCT
                                                                                                                             CCTCATCAATATCCGCCATCCCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTA
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 GCCCATCTGGTACCACTGCCGCCGCCCCAGATACCTGTCATCGGTCATGTGTGTCCTGCT
                                                                                                                                                                                          20.9%; ilarity 99.8%; Conservative
                                                                                                                                                                                          Score 546; DB 4; Length 969; Pred. No. 1.2e-228; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6492505 1909132CT1
US-09-495-050A-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-495-050A-164
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CURRENT FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: February 1, 1999
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 164
LENGTH: 291
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APPLICANT: Roopa, Reddy
APPLICANT: Gougler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
FILE REFERENCE: PA-0013 US
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 291; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 164, Application US/09495050A Patent No. 6492505
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                                                                                    CTGGGCCCTGTCCCTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAG
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                                                                                                                                                                                                                                                                                                100.0%;
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100.0%; Pred. No. 2.4e-117;
rive 0; Mismatches 0;
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US-09-016-434-330
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 33
SEQUENCE CHARACTERISTICS:
LENGTH: 275 base pairs
TYPE: nucleic acid
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APPLICANT: Jeffrey J. Sellhamer
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
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TORARY: CONNTUTO1
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PRIOR APPLICATION NUMBER:
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MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
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CORRESPONDENCE ADDRESS:
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CLONE: 1909132
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STATE: CALIFORNIA
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                                                            CTGCTGCGGAGTATCCTGGAGTGGATTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT 1001
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3174 PORTER DRIVE
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SOPTWARE: PatentIn vers
SEQ ID NO 10
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
US-09-254-227A-10
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SEQ ID NO 8
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; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-254-227A-8
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APPLICANT: Ahmad, St.
APPLICANT: Banville,
APPLICANT: Fortin,
APPLICANT: Lembo, Pa
                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09254227A Patent No. 6696257 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                           APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
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APPLICANT: Lembo, Paola
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Heiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
                                                                                                                         NUMBER OF SEQ ID NOS:
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Banville, Denis
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Banville, Deni
Banvin, Yves
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                                                                                                        PatentIn version 3.0
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Pred. No. 1.7e-68;
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1350 859 1410

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; SOFTWARE: PatentIn vers
; SEQ ID NO 14
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-254-227A-14
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US-09-254-227A-12
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Best Local Similarity 100.
Matches 97; Conservative
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TITLE OF INVENTION: G PROFUN-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/266117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 969
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09254227A Patent No. 6696257
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Patent No. 6696257
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Query Match
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APPLICANT:
APPLICANT:
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                                                                                                                                   APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: Uembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors
FILE REFERENCE: 81823/288117
CURRENT APPLICATION NUMBER: US/09/254,227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
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                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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Fortin, Yves
                                                                                                                      PatentIn version 3.0
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Fortin, Yves
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Lembo, Paola
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Conservative (
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3.1%;
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 Score 80;
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 DB 4;
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Length 969;
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GENERAL INFORMATION:
APPLICANT: Huang, Tim
APPLICANT: Huang, Tim
FILE REFERENCE: UMO1523
CURRENT APPLICATION NUMBER: US/09/497,855A
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/120,592
PRIOR APPLICATION NUMBER: 60/118,760
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARDE. DEFORT OF SERVICE SERVIC
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US-09-497-855A-32/c
; Sequence 32, Application US/09497855A
; Patent No. 6605432
; Patent No. 6605432
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US-09-918-686-1/c
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Best Local Similarity 100.0%;
Matches 31; Conservative (
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Query Match 1.1%; Score 30; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 30; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Proll, Sean
APPLICANT: Paeper, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brunkow, Mary
                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: 7043, 8369, 8401
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 92139
TYPE: DNA
                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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                                   DB 4; 1
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   <u>.</u>
                                                                      Length 92139;
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; Sequence 2, Application US/09346510B
; Patent No. 6281014
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Wang, Yinxiang
; TITLE OF INVENTION: SH3-Containing Protein, DN
; FILE REFERENCE: D6221CIP
; CURRENT FILING DATE: US/09/346,510B
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/871,732
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                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: LINEAR MOLECULE TYPE: OTH
                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
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LENGTH: 735 BASE PAIRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: MCGREGOR, MARTIN L.
REGISTRATION NUMBER: 29,339
REFERENCE/DOCKET NUMBER: 1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: O'BRIEN, TIMOTHY J. APPLICANT: WANG, YIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 713-682-1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FITLE OF INVENTION: CELLS, VECTORS AND FITTLE OF INVENTION: PROTEIN, ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 713-682-5807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UI
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180 WEST 34TH STREET, #345
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100.0%; Prr
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US-07-972-481-1
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                                                                 US-07-972-481-1
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Best Local Similarity
Matches 24; Conserv
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LENGTH: 735
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                                Query Match
                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: INTERNATIONAL PCT/
FILING DATE: 09-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SVENSON, LEONARD R
REGISTRATION NUMBER: 300
REFERENCE/DOCKET NUMBER: 446-102PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                TELEFAX: (703) 205 80:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
CHOCKERSTON. CDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: CLONING AND EXPRESSION OF TOXOPLASMA ANTIGENS NUMBER OF SEQUENCES: 4

CORRESPONDENCE: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,481
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 682 base pairs
                                                                                                                  FEATURE:
                                                                                                                                   MOLECULE TYPE:
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                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                             LENGTH: 682 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: FALLS CHURCH
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ZIP: 22040-0747
                                                                                                                                                 TOPOLOGY:
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8110 GATEHOUSE ROA
                                                                                                                                                                                                                                                 (703) 205 8050
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 Conservative
                                                                                                                                                  linear
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                                                                                                                                 DNA (genomic)
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                   Score 24;
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                 DB 1;
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RESULT 14
US-09-149-476-179
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GENERAL INFORMATION:
APPLICANT: Rosen et
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APPLICATION NUMBER: 60/038,621
PTITING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,600
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APPLICATION NUMBER: 60/040,162
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APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
                                                                                                                           APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/047,581 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,584
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ETTING DATE: 1997-05-23
ETTING DATE: 1997-05-23
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                                                                                                                                                                             APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                    FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
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APPLICATION NUMBER: 60/047,598
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APPLICATION P
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APPLICATION NUMBER: 60/047,587
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APPLICATION NUMBER: 60/056,893 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313 APPLICATION NUMBER: 60/043,314 FILING DATE: FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,894 APPLICATION NUMBER: 60/056,903 FILING DATE: FILING DATE: 1997-08-22 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/043,674 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11 FILING DATE: 1997-04-11 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,568 APPLICATION NUMBER: 60/056,911 FILING DATE: FILING DATE: FILING DATE: APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 APPLICATION NUMBER: APPLICATION NUMBER: 60/056,889 APPLICATION NUMBER: 60/056,877 FILING DATE: FILING DATE: APPLICATION NUMBER: 60/043,671 APPLICATION NUMBER: 60/043,311 APPLICATION NUMBER: 60/056,880 APPLICATION NUMBER: 60/056,888 FILING DATE: APPLICATION NUMBER: 60/056,872 APPLICATION NUMBER: 60/056,662 FILING DATE: APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-04-11 FILING DATE: ON NUMBER: 60/056,864 NUMBER: 60/056,845 NUMBER: 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-08-22 1997-04-11 1997-04-11 1997-04-11 1997-04-1 R: 60/056,892 60/056,879 60/056,630

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Query Match
Best Local Similarity
Matches 24; Conserv
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APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
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FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/056,884
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APPLICANT: Jobert, S.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET: 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 14560

LENGTH: 87
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                                                                                                            ; TYPE: DNA; ORGANISM: Homo sapiens US-09-621-976-14560
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Search completed: October 30, 2004, 00:50:23
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ALIGNMENTS

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Publication No. US20040076951A1

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al.

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 2618; Conserv
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL000900-CIP
CURRENT APPLICATION NUMBER: US/09/867,570
CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/695,045
PRIOR FILING DATE: 2000-10-25
121 CACCAGGATTGGAAGCTTCCTGAGGCCTCCCCAGAAGCAGAAGCTGCTATGCTTCTTGTA 180
                                                                             61
                                                                                                                                                1 AACAATTGCCGCGAATTCGGCCACGAGATGAAATCTAGTTGTTTAAAAAGCGTGTAGCACCT
                                                              CCTCCCTCTCTTACTCCTGCTCTCACCATGTGAGACGCCTCGCCTCCCCCCTTTGCCTTT
                                                                                                                         AACAATTGCCGCGAATTCGGCACGAGATGAAATCTAGTTGTTTAAAAGCGTGTAGCACCT
                                                                                                                                                                                                100.0%; Score 2618; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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GETTETTIRAGCANTTMACCASTTANACCANTTTCCTTCATANATTTCCCAGTCTCAGG ATTETTTTTTTTTTTCAGANTTANACCANTTTCCTTCATANATTTCCCAGTCTCAGG ATTETTTTTTTTTTTCAGANTTANACCANTTTCCTTCAGANTANACCAAGAGG CCCAAAGTGCTTTCCTTCTTCTTCTTCTTCTTCTTCAGTTCTTCAGATTTCCCAGTCTTCAGA ACCACAGANACCAGANATTANAAAGANTCCCACTCTCTTCTTCTTCAGTTCAG	GAGGECATEA 7 TETECCAAAA 7 TETECCAATA 7 TETECAATA 7 TETECCAATA 7 TETECCAATA 7 TETECCAATA 7 TETECCAATA 7 TETECC

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Qy 526 TGACACCAATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGG 585	US-09-867-570-3 US-09-867-570-3 Sequence 3, Application US/09867570 ; Sequence 3, Application US/09867570 ; Publication No. US20040076951A1 ; GENERAL INFORMATION: APPLICANT: WEI, Ming-Hui et al. APPLICANT: WEI, Ming-Hui et al. TITLE OF INVENTION: INCLETC ACID MOLECULES ENCODING HUMAN GPCR TITLE OF INVENTION: PROTEINS, AND USES THEREOF FILE REFERENCE: CL000900-CIP ; CURRENT FILING DATE: 2001-05-31 ; PRIOR FILING DATE: 2001-05-31 ; PRIOR APPLICATION NUMBER: US/09/655,045 PRIOR FILING DATE: 2000-10-25 ; NUMBER OF SEQ ID NOS: 4 ; SOFTMARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 3 ; LENGTH: 8622 ; TYPE: DNA ; SOFTMARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 3 ; LENGTH: 8622 ; TYPE: DNA ; OP-867-570-3 QUERY Match Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0; Matches 1101; COnservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1101; COnservative 0; Mismatches 0; Todels 525 QY 466 GGGTCATCAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAAC 525	Qy 2341 TAGTTTTATGGCTGTTTACATGAGAAGCAAAACATCTGACCATGACAA 2400
RESULT 3 (Sequence 1273, Application US/10292798) (Sequence 1273, Application US/10292798) (Publication No. US20030235833A1) (GENERAL INFORMATION: (APPLICANT: SUWA, MAKIKO APPLICANT: AKIYAMA, YUTAKA APPLICANT: ASUXATANI, HIROYUKI (APPLICANT: ABUXATANI, HIROYUKI (TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS (CURRENT APPLICATION NUMBER: US/10/292,798 (CURRENT APPLICATION NUMBER: US/10/292,798 (CURRENT APPLICATION NUMBER: US/10/292,798 (CURRENT FILING DATE: 2001-12-18 (PRIOR APPLICATION NUMBER: J0/017,161 (PRIOR PILING DATE: 2001-12-18 (PRIOR PILING DATE: 2001-166-18 (NUMBER OF SEQ ID NOS: 2070 (SOFTWARE: Patentin Ver. 2.1 (SEQ ID NO 1273 (LENGTH: 1369)	Qy 1186 TTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGAATTGAAAGTCTTATTTTGTC 1245	Db 7862 TGCTGAGCGCCAGATACCTGTCATCGTTGCATCCTTGTGGCCCATCTTTTTTTT

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; NAME/KEY: CDS
; LOCATION: (201)..(1169)
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Best Local Similarity 99.8%;
Matches 1193; Conservative
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LOCATION: source
FEATURE:
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ORGANISM: Homo sapiens
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                                ATGTGCATCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTT 1305
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           ACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCC
                                                                                  TTGGCATTCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTC 1245
                                                                                                                          CCAGGCTGTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCCTCTTGTGGGCCTGCCCT 1185
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TYPB: DNA
COGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (332)...(1297)
US-10-183-116-30
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Sequence 30, Application US/10183116
Publication No. US20030092035A1
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Eyka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
ITITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE, 4C1CP1
CURRENT APPLICATION NUMBER: US/10/183,116
CURRENT APPLICATION NUMBER: US 60/222,344
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/205,493
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEO 110 NOS-109
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Best Local Similarity 100.0%; F
Matches 1088; Conservative 0;
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 30
                                                                                                                                                                                                                                                                     CAGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACC
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GTGCATCGTTTCCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCT
                              GTGCATCGTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTG
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f; Pred. No. 0;
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RESULT 5
US-10-225-567A-673
US-10-225-567A-673
Sequence 673, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
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APPLICANT: Burmer, Glenna C.
APPLICANT: ROUSH, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIFICE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIFICE OF THE REPERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 673
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-673
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Local Similarity 100.0%; Pred. No. 0;
hes 1088; Conservative 0; Mismatches
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; CTHER INFORMATION: No. US20020193584Alel Sequence US-09-995-225-19	; TYPE: DNA ; ORGANISM: Artificial Sequence	; SOFTWARE: PatentIn version 3:1 ; SEQ ID NO 19 ; LENGTH: 969	ING DATE: 2001-07-31 SEQ ID NOS: 67	PRIOR FILIDATION NUMBER: 60/309,208	APPLICATION NUMBER: 60/282, APPLICATION NUMBER: 60/282, APPLICATION NUMBER: 60/282			FILING DATE: 2001-02-20 APPLICATION NUMBER: 60/282, FILING DATE: 2001-04-06			E C z C	GENERAL INFORMATION: APPLICANT: Chen, Ruoping APPLICANT: Chu, Zhi Liang APPLICANT: Chu, Zhi Liang	RESULT 6 US-09-995-225-19 US-09-995-225-19 Sequence 19, Application US/09995225	Db 1393 CAGAAATG 1400	133 GAGAGCATGCCCTGCCACCCTTGACAATTATATGCATTTTCTTAGCCTTCTGCCT 139	143 GCTGTCGGGAAGCAGATTGGAGCAGTGAGAACCTCTGCCCTGTCAGACAGGACTTT 1273 GCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTT 1273 GCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGTCCTGAGACAGGACCTTTT 1483 GAAACCAAGGACGGCCCGAACCCGTTTTAACAATATTATTATTTTTTTT	133 1C1GCAGACACGCC SANGS SGALIGARAGG SGAGGG SGC11C1CAGGAAACCCC1GGAGACACGACGAGGAGAGGGGGGGCTTCCTCAGGAAACCCCTGGAGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCCTGGA	1313 TOTTOCAGA CAGAGA CAGAGAGAGAGAGAGAGAGAGA A AGAGAGAG	1093
Db 961 GAGCAGTGA 969	Qy 1452 GAGCAGTGA 1460	Oy 1392 GTGGATGAAGGTGGAGGGTGCTTCCTCAGGAAACCCTGGAGGTGTCGGGAAGCAGATTG 1451 Db 901 GTGGATGAAGGTGGAGGGTGCCTCCTCAGGAAACCCTGGAGCTGTCGGGAAGCAGATTG 960	841 CGTCAAAATAGGCAGAACCTGAAGCTTGGTTCTCCAGAGGGCTCTGCAGGACACGCCTGAG	Qy 1332 CGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACACGCCTGAG 1391	Db 781 TCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAG 840	721	Qy 1212 AGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTTCCATTTTCCTG 1271	Qy 1152 ACAGTGCTGGTCTTCCTCCTCTGTGGCCTTTTGGCATTCAGTGGGCCCTGTTTTCC 1211	Qy 1092 AGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGACCATCCTCCTC 1151	Qy 972 TGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAGATTTCATTACA 1031	Qy 912 GTCATGTGTGTCCTGCTCTGGGCCCTGTCCCTGCGGAGTATCCTGGAGTGGATGTTC 971	OY 852 TGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCCCAGATACCTGTCATCG 911	QY 792 GTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCAGCACCGAGCGC 851	QY 732 ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCCAACATCCTCAGTCCT 791	OY 672 GTCTCCATCTACATCCTCAACCTGGTCGCGGCCGACTTCCTTC	Qy 612 GCGCTGACAGGAAACGCGGTTGTGCTCTGGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT 671	QY 552 ACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGACGTGCATCGTTTCCCTTGTC 611	Qy 492 ATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACCAATCAACGGACGTGAGGAG 551	Query Match 37.0%; Score 969; DB 9; Length 969; Best Local Similarity 100.0%; Pred. No. 0; Matches 969; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-19
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CURRENT PILLING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR PILLING DATE: 1998-10-13
PRIOR PILLING DATE: 2000-1-27
PRIOR PILLING DATE: 2000-1-27
PRIOR PILLING DATE: 2000-12-12
PRIOR PILLING DATE: 2001-02-20
PRIOR PILLING DATE: 2001-02-20
PRIOR PILLING DATE: 2001-04-06
PRIOR PILLING DATE: 2001-04-06
PRIOR PILLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR PILLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR PILLING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/270,266
PRIOR PILLING DATE: 2001-02-20
PRIOR PILLING DATE: 2001-04-06
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SEQ ID NO 19
LENGTH: 969
TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 969; Conserv
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APPLICANT: Chu, I
APPLICANT: Dang,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/290,917
PRIOR FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: 60/309,208
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lowitz, Kevin P.
APPLICANT: Pride, Cameron
TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: AREN-0308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/282,358
FILING DATE: 2001-04-06
APPLICATION NUMBER: 60/282,356
FILING DATE: 2001-04-06
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Chu, Zhi Liang
Dang, Huong T.
Lowitz, Kevin P.
Pride, Cameron
                                                    ATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCATCTCCAAAATCCTCAGTCCT 791
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%; Pred. No. 0;
0; Mismatches
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                                                                                                                              Sequence 1, Application US/10401397A

Publication No. US20030212001A1

GENERAL INFORMATION:
APPLICANT: Peri, Krishna G.
APPLICANT: Moffett, Serge
APPLICANT: Moffett, Serge
APPLICANT: Moffett, Serge
APPLICANT: Moffett, Serge
APPLICANT: MOFFET, Daniel
TITLE OF INVENTION: INTRAOCULAR PRESSURE AND RELATED CONDITIONS
FILE REFERENCE: 4518/1M674US1
CURRENT APPLICATION NUMBER: US/10/401,397A
CURRENT APPLICATION NUMBER: US 60/367,513
PRIOR APPLICATION NUMBER: US 60/367,513
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US-10-401-397A-1
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; ORGANISM: Homo
US-10-391-074-1
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US-10-391-074-1
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APPLICANT: Wattler, Frank
APPLICANT: Wattler, Frank
APPLICANT: Wattler, Frank
TITLE OF INVENTION: NO. US20040038345A1el Human Seven-Transmembrane Receptors
FILE REFERENCE: 7705,0008-00-000
CURRENT APPLICATION NUMBER: US/10/391,074
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 969
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Publication No. US20040038345A1
GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 917; Conservative
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                  ACAGIGCIGGICITCCICCICIGIGGCCIGCCCITIGGCATICAGIGGGCCCIGITITICC 1211
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Pred. No. 0;
0; Mismatches
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US-10-219-834-7
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PRIOR FILLING DATE: 2001-10-30
PRIOR PELICATION NUMBER: US 60/318,675
PRIOR APPLICATION NUMBER: US 60/315,596
PRIOR APPLICATION NUMBER: US 60/355,596
PRIOR FILLING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US 60/333,417
PRIOR FILLING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: US 60/338,367
PRIOR FILLING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 192
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Best Local Similarity 100.0%; Pred. No. 0;
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LENGTH: 1997
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ORGANISM: Homo sapiens
-10-219-834-7
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CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/313,658
PRIOR FILING DATE: 2001-08-20
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TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF
FILE REFERENCE: D0191 NP
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RESULT 11
US-10-237-467-9
GENERAL INFORMATION:
                         Sequence 9, Application US/10237467 Publication No. US20030186324A1
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CURRENT APPLICATION NUMBER: US/10/237,467
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/317,879
PRIOR FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                              Matches
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liao, Jiayu
APPLICANT: Gray, Nathanael S.
APPLICANT: Galdwell, Jeremy C.
APPLICANT: Schultz, Peter G.
APPLICANT: IRM LLC
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Sensory Neuron Receptors FILE REFERENCE: 021288-001300US
                                                                                                                                                             OTHER INFORMATION: dorsal root ganglia G-protein coupled receptor (GPCR) OTHER INFORMATION: 7 (DRG7) (NT009307)
                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                            LENGTH: 909
TYPE: DNA
                                                                                 Local
612 GCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTGCCGCATGCGCAGGAACGCT
                                                            al Similarity
847; Conserv
                                                            28.5%;
llarity 99.8%;
Conservative
                                                            Score 747; DB; Pred. No. 0; O; Mismatches
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Indels

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; Sequence 239, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
   APPLICANT: WANG, YIXIN
   TITLE OF INVENTION: EXPRESSION PROFILES AND ME:
   FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
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; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: modified_base
; LOCATION: (750)
; OTHER INFORMATION: a, t, C
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; SEQ ID NO 239
; LENGTH: 769
; TYPE: DNA
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              GACAGGACTTTGAGAGCAATGCTGCCCTG 1510
                                                                   GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCA
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                                                    GAAACCCTGGAGCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCA
                                                                                                           CTCCAGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAG
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RESULT 13
US-10-017-161-1599
; Sequence 1599, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:

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; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: AKUYAMA, YUTAKA
; APPLICANT: AKUYAMA, YUTAKA
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/01.52
; CURRENT APPLICATION UNUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 1599
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; NAME/KEY: CDS
; LOCATION: (996)..(1170)
US-10-017-161-1599
                                                                               Sequence 164, Application US/10313542
Publication No. US20030120057A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 1.2e-210;
Matches 434; Conservative 0; Mismatches 0;
APPLICANT: Roopa, Reddy
APPLICANT: Guegler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OP INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (201)..(619)
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LOCATION: (1)..(1370)
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CGCCATCCCATCTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA

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CURRENT APPLICATION NUMBER: US/10/313,542
CURRENT FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: US/09/495,050
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/118,318
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 305
SOPTWARE: PERL Program
SEQ ID NO 164
LENGTH: 291
                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 1909132
US-10-305-720-330
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 330
LENGTH: 275
TYPE: DNA
CONCENTED: 1998-01-30
LENGTH: 275
TYPE: DNA
CONCENTED: CONCENTED: 1998-01-30
LENGTH: 275
TYPE: DNA
CONCENTED: CONCENTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 330, Application No. US206
GENERAL INFORMATION:
                                                                                                                  Query Match
Best Local Similarity
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030120057A1 1909132CT1
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ORGANISM: Homo sapiens
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CGCCATCCCAAAATCCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTA
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                                                                                       Conservative
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hive 0; Mismatches
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                                                                                                               Score 275; DB 16; 1
Pred. No. 2.3e-129;
                                                                                           Mismatches
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Search	뮹	Ą	Db	Ŋ	Дb	Ş	Db ·	Ş
Search completed: October 30, 2004, 03:54:26 Job time : 1230 secs	Db 241 GTTTGGTGTAAACGTCAGATTTCATTACAATCGC 275	Qy 1002 GTTTGGTGTGAAACGTCAGATTTCATTACAATCGC 1036	Db 181 CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT 240	Qy 942 CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT 1001	Db 121 CACTGCCGCCCCAGATACCTGTCATCGGTCATGTGTGTGT	Qy 882 CACTGCCGCCCCCAGATACCTGTCATCGGTCATGTGTGTG	Db 61 AGCATGCTGAGCGCCATCAGCACCGAGCGCTGTCCATCCTGTGGCCCATCTGGTAC 120	Qy 822 AGCATGCTGAGCGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTAC 881

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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2618
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m2_6/ptodata/1/pna/US081_COMB.seq:*
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m2_6/ptodata/1/pna/US083_COMB.seq:*
m2_6/ptodata/1/pna/US083_COMB.seq:*
m2_6/ptodata/1/pna/US083_COMB.seq:*
m2_6/ptodata/1/pna/US084_COMB.seq:*
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gn2_6/ptodata/1/pna/US086_COMB.seq:*
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gn2_6/ptodata/1/p
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6_COMB.seq:*
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45: 'cgm2-6', ptodata/1', pna/(US100A_COMB. seq: 46; 'cgm2-6', ptodata/1', pna/(US100A_COMB. seq: 47; 'cgm2-6', ptodata/1', pna/(US101A_COMB. seq: 48; 'cgm2-6', ptodata/1', pna/(US101A_COMB. seq: 49; 'cgm2-6', ptodata/1', pna/(US1001_COMB. seq: 49; 'cgm2-6', ptodata/1', pna/(US1012_COMB. seq: 49; 'cgm2-6', ptodata/1', pna/(US1012
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HUMAN

GPCR

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117:
118:
119:
120:
121:
122:
122:
123:
124:
125:
/cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US6054_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6059_COMB.seq:*
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Pred. is derived by analysis of the total score distribution. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed,

SUMMARIES

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 C 10 6 5 4 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
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ALIGNMENTS

RESULT 1
US-09-867-570-1
; Sequence 1, Application
; GENERAL INFORMATION:

US/09867570

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; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 1
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: Human
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TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLES ENCODING
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000990-CIP
CURRENT PEDLICATION NUMBER: US/09/867,570
CURRENT FILING DATE: 2001-05-31
CHRENT FILING DATE: 2001-05-31
PRIOR PELING DATE: 2001-025
PRIOR FILING DATE: 2001-025
PRIOR FILING DATE: 2001-025
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us;	1801 CCTGATAGTATCAAAAAGGAAGATTCCTTATTAATCTGTCAGACTATGTTCCCCTGAAAA 1860
	TTGTTTCCTA 1
	1681 ACATTTTCCCTGTTATCTTGCACTGAATCTTTTCCTACTGAACACTTTTTCTGCACTTTTC 1740
	1621 CACCCATGGAAAGCATTAGTCTGACAGTACAATGTTTGGATTCTCCTTGATATTACCAAT 1680
RE:	1561 TCTCAGTGGTCCCTCAAGGTCTTCGAATAGATGTTTATCTAACCTGACAGTTGCAGTTTT 1620
Db S	1501 TGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCTCAGAAATG 1560
? B 4	1441 GAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTTGAGAGCAA 1500
D 4	1381 ACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCTGGAGCTGTCGG 1440
S B 4	1321 CCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGG 1380
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Q D 4	1201 CCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCATCTAGTTT 1260
0 B	1141 CCATCCTCACAGTGCTGGTCTTCCTCCTCTGTGGCCTGCCCTTTGGCATTCAGTGGG 1200
? B &	1081 TCCTGCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCTGTACGTGA 1140
D &	1021 ATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGGTTCTCTGTGGGGTCCAGCCTGG 1080
2 D 43	961 AGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGAAACGTCAG 1020
₽ Q	901 ACCTGTCATCGGTCATGTGTGTGTGCTCTGGGCCCTGTCCCTGCCGGAGTATCCTGG 960
2 B &	841 GCACCGAGCGCTGCCTGTCCATCCTGTGGCCATCTGGTACCACTGCCGCCGCCCCAGAT 900
	781 TCCTCAGTCCTGTGATGACCTTTCCCTACTTTATAGGCCTAAGCATGCTGAGCGCCATCA 840

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           AGGAGGATCCTGGTGCTGGAAAAAAAAAAAAAAAAAAA 2618
                                                                  TCTCAATTATGGTATCTGGATAATAACTTACAGTTGGTACAGAATTCTGATACATGCTGT
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US-60-190-928-1
US-60-190-928-1
; Sequence 1, Application US/60190928
; General Information:
; APPLICANT: Bonazzi, Vivien
APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTOR HAVING HOMOLOGY TO THE MAS PROTO-ONCOGENE, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING THIS HUMAN GPCR PROTEIN, AND USES
; TITLE OF INVENTION THEREOF
; FILE REFERENCE: CL000387
; CURRENT APPLICATION NUMBER: US/60/190,928
; CURRENT FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: HUMAN
US-60-190-928-1
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181 CAGTCTGTAGAGCTATTAGCCAGTTAAACCCATTTCCTTCATAAATTTCCCAGTCTCAGG	Db 61 CCTCCCTTACTCCTGAGGCCTCCCAGAAGCAGAAGCTGCTATGCTTCTTGTA 180 Db 121 CACCAGGATTGGAAGCTTCCTGAGGCCTCCCCAGAAGCAGAAGCTGCTATGCTTCTTGTA 180 Db 121 CACCAGGATTGGAAGCTTCCTGAGGGCTCCCCCAGAAGCAGAAGCTGCTATGCTTCTTGTA 180 Db 121 CACCAGGATTGGAAGCTTCCTGAGGGCCTCCCCAGAAGCTGCTATGCTTCTTGTA 180	1 AACAATTGCCGCGAATTCGGCACGAGATGAAATCTAGTTGTTTAAAAGCGTGTAGCACCT	Query Match 100.0%; Score 2618; DB 84; Length 2618; Best Local Similarity 100.0%; Pred. No. 0; Matches 2618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; LENGTH: 2618 ; TYPE: DNA ; ORGANISM: HUMAN US-60-190-928-1	CURRENT FILING DATE: 2000-03-21 NUMBER OF SEQ ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 4.0 SEO ID NO 1	NTION: ACID MOLECULES ENCODING THIS HUMAN GPCR PROTEIN, AND NTION: THEREOF E: CLOO387 CATTON NUMBER: 118/60/190 928	ATION: nazzi, Vivien NTION: TSOLATED HUMAN G-PROTEII NTION: RECEPTOR HAVING HOMOLOGI	Sequence 1. Application US/60190928	Qy 2581 AGGAGGATCCTGGTGCTGGAAAAAAAAAAAAAAAAAAAA	OY 2521 GTAAGTTCAAATTCTATGAGGTATCCAAATTAGGAAATTCTTGAACACAGAAAATAAAT	QY 2461 GACATACATGAACCTGGAAATATTTGTGCTAAGGAAAATAAGCCAGACGCCAAACAATATT 2520	QY 2401 TCTCAATTATGGTATCTGGATAATAACTTACAGTTGGTACAGAATTCTGATACATGCTGT 2460	QY 2341 TAGTTTTATGGCTGTTTACATGAGAAGCAAAACTGAAAACATCTGACCTTTCCATGACAA 2400	Qy 2281 GTAGGAGAATTCTTCATACTTCCAGGTTTTGTATAAATTGTTCTGATTGTAACTTTCAGT 2340	Qy 2221 ATTTIAAAGTGGAAATTATCTTGAAAACCATTTATTATTCACTTACAGATTCTTTCAGTT 2280	Qy 2161 TGAGGAGCCTATAAATATGTCCCACCAGTTTCATTTTTGGCCATTGGAAACCTCAATATTG 2220
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Sequence 4370, Application US/09721588

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2046-001
CURRENT APPLICATION NUMBER: US/09/721,588
CURRENT FILING DATE: 12000-11-22
PRIOR APPLICATION NUMBER: 60/167,381
PRIOR FILING DATE: 1299-11-24
NUMBER OF SEQ ID NOS: 5410
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 4370
LENGTH: 1453
TYPE: DNA
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RESULT 5
US-09-634-7540-740
Sequence 740, Application US/09634754
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: AL-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DETECTING EXPRESSION OF GENES ENCE FILE REFERENCE: PA-0017 US
CURRENT APPLICATION NUMBER: US/09/634,754
CURRENT APPLICATION NUMBER: US/09/634,754
CURRENT FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: 287, 299, 301, 305, 325
NAME/KEY: unsure
LOCATION: 395, 399, 407
OTHER INFORMATION: a or g or c or
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No:
PUBLICATION INFORMATION:
US-09-634-754-740
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Best Local Similarity 100.0%;
Matches 1147; Conservative (
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                                                       GGACTTTGAGAGCCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTTCTTAGCCT
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APPLICANT: Lal, Preeti
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APPLICANT: Guegler, Karl J.

APPLICANT: Guegler, Karl J.

APPLICANT: Baughn, Mariah R.

APPLICANT: Shah, Purvi
ITILE OF INVENTION: DETECTING EXPRESSION OF GENES ENCODING SECRETED PROTEINS
FILE REFERENCE: PA-0017 US
CURRENT APPLICATION NUMBER: US/09/634,754D
CURRENT FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 809
SOFTWARE: PERL Program
SEQ ID NO 740
LENGTH: 1557
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 287, 299, 301, 305, 325, 329-330, 350-351, 361, 366, 371, 377
FEATURE:
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OTHER INFORMATION: Incyte ID
PUBLICATION INFORMATION:
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| Sequence 740, Application US/10745444
| GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: 395, 399, 407
OTHER INFORMATION: a or g or
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte II
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APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Shah, Purvi
                                                                                                                      FEATURE:
NAME/KEY: unsure
LOCATION: 287, 299,
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SOFTWARE: PERL Program

SEQ ID NO 55

LENGTH: 1146

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 338589.1
US-09-532-367-55
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GENERAL INFORMATION:
APPLICANT: Hodgson, David M.
APPLICANT: Lincoln, Stephen E.
APPLICANT: Lincoln, Stephen E.
APPLICANT: Spiro, Peter A.
APPLICANT: Banville, Steve C.
APPLICANT: Banville, Steve C.
APPLICANT: Bearcher, Shawn R.
APPLICANT: Dufour, Gerard E.
APPLICANT: Cohen, Howard J.
APPLICANT: Cohen, Howard J.
APPLICANT: Chalup, Michael S.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yu, Jimmy Y.
APPLICANT: Greenawalt, Lila B.
APPLICANT: Panzer, Scott R.
APPLICANT: Roseberry Ann M.
APPLICANT: Roseberry Ann M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROSEberry, Ann M.
APPLICANT: Wright, Rachel J.
TITLE OF INVENTION: RECEPTOR MOLECULES
FILE REFERENCE: PT-0005 US
CURRENT APPLICATION NUMBER: US/09/532,367
CURRENT FILING DATE: 2000-03-21
EARLIER REPLICATION NUMBER: 60/125,366; 60/126,218; 60/126,247; 60/126,590; 60/125,79:
EARLIER FILING DATE: 1999-03-19; 1999-03-25; 1999-03-24; 1999-03-26; 1999-03-23;
NUMBER OF SEQ ID NOS: 63
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CTGCTGCGGAGTATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCT
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RESULT 10
US-09-867-570-3
US-09-867-570-3
(Sequence 3, Application US/09867570
(SEQUENCE INFORMATION:
(APPLICANT: WEI, Ming-Hui et al.
(TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
(TITLE OF INVENTION: PROTEINS, AND USES THEREOF
(FILE REFERENCE: CL000900-CIP
(CURRENT APPLICATION NUMBER: US/09/867,570)
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; PRIOR APPLICATION NUMBER: 09/695,045
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.
; SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 3
; LENGTH: 8622
; TYPE: DNA
; ORGANISM: Human
US-09-867-570-3
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

ITILE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

ITILE OF INVENTION: PROTEINS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/60/201,715

CURRENT APPLICATION NUMBER: US/60/201,715

CURRENT FILING DATE: 2000-05-03

NUMBER OF SEQ ID NOS: 124

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 47

LENGTH: 3988

TYPE: DNA

ORGANISM: HUMAN

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                                                                              Sequence 1273, Application US/10292798

GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KYOSHI
APPLICANT: ASAI, KYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKIYAMA, YUTAKA
CURRENT APPLICATION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 08435/166
CURRENT APPLICATION UNMBER: US/10/292,798
CURRENT APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2011-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1273
LENGTH: 1369
TYPE: DNA
ORGANISM: Homo sapiens
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                              AGAGGGCTCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAA
                                                                        ACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCC
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Pred. No. 1.2e-226;
0: Mismatches 2;
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APPLICANT: Simon, Melvin
APPLICANT: Simon, Melvin
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.004VPC
CURRENT PILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-04-19
NUMBER OF SEQ ID NO3 1
SEQ ID NO 30
LENGTH: 1400
TYDE: DNA
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; LOCATION: (332)...(1297)
PCT-US01-14519-30
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Best Local Similarity
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ORGANISM: Homo :
FEATURE:
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RESULT 14
PCT US03-15004-30
; Sequence 30, Appl;
; GENERAL INFORMATI
; APPLICANT: Calii
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; APPLICANT: Syll
APPLICANT: California Institute of Technology
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Sylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C10PC
CURRENT APPLICATION NUMBER: PCT/US03/15004
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION UMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
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SOFTWARE: PRETSEQ for Windows
SEQ ID NO 30
LENGTH: 1400
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Best Local Similarity 100.0%; Pred. No. 1.4e-225;
Matches 1088; Conservative 0; Mismatches 0;
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ORGANISM: Homo :
FEATURE:
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Qy 653 CCGCATGCGCAGGAACGCTGTCCCATCTACATCCTCAACCTGGTCGCGGCCGACCTTCCT 712	Qy 593 GTGCATCGTTTTCCCTTGTCGCGCTGACAGGAAACGCGGTTGTGCTCTGGCTCCTGGGCTG 652	Qy 533 AATCAACGGACGTGAGGAGACTCCTTGCTACAAGCAGACCCTGAGCTTCACGGGGCTGAC 592	AGACTGGGGTTTCTGAGCATGGATTCAACCATCCCAGTCTTGGGTACAGAACTGACACC 53 	Query Match 41.6%; Score 1088; DB 35; Length 1400; Beet Local Similarity 100.0%; Pred. No. 1.4e-225; Matches 1088; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURE: NAME/KEY: CDS LOCATION: (332)(1297) S-09-849-869A-30	. . .	PRIOR PRIOR NUMBER	PRIOR FILING DATE: PRIOR APPLICATION N PRIOR APPLICATION N PRIOR FILING DATE:	CURRENT APPLICATION NUMBER: US/09/849,869A CURRENT FILING DATE: 2001-05-04 PRIOR APPLICATION NUMBER: US 60/222,344 PRIOR APPLICATION NUMBER: US 60/222,344		GENERAL INFOI APPLICANT: J APPLICANT:	RESULT 15 US-09-849-869A-30 . Someone 30 Application US/00040860A	Qy 1553 CAGAAATG 1560 Db 1393 CAGAAATG 1400	Qy 1493 GAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCT 1552	OY 1433 GCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTT 1492	Oy 1373 TCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGTGGCTTCCTCAGGAAACCCTGGA 1432	Db 1153 CGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCCAGAGGGC 1212
		Search completed: October 30, 2004, 03:30:29 Job time : 9593 secs	Qy 1553 CAGAAATG 1560 Db 1393 CAGAAATG 1400	Db 1333 GAGAGCAATGCTGCCCCCGCCACCCTTGACAATTATATGCATTTTCTTAGCCTTCTGCCT 1392	1433 GCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTT	Qy 1373 TCTGCAGGACACGCCTGAGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCTGGA 1432	Qy 1313 CGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGC 1372	OY 1253 TCTAGTTTCCATTTTCCTGTCCGCTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTT 1312	QY 1193 TCAGTGGGCCCTGTTTTCCAGGATCCACCTGGATTGGAAAGTCTTATTTTGTCATGTGCA 1252	OY 1133 GTACGTGACCATCCTCCTCACAGTGCTGGTCTTCCTCTGTGGCCTGTGGCCTTTGGCAT 1192	OY 1073 CAGCCTGGTCCTGGTCAGGATTCTCTGTGGATCCCGGAAGATGCCGCTGACCAGGCT 1132	Qy 1013 AACGTCAGATTTCATTACAATCGCGTGGCTGGTTTTTTTATGTGTGGTTCTCTGTGGGTC 1072	Qy 953 TATCCTGGAGTGGATGTTCTGTGACTTCCTGTTTAGTGGTGCTGATTCTGTTTGGTGTGA 1012	Qy 893 CCCCAGATACCTGTCATCGGTCATGTGTGTGTGTGGGGCCCTGTCCCTGCCGGAG 952	Qy 833 CGCCATCAGCACCGAGCGCTGCCTGTCCATCCTGTGGCCCATCTGGTACCACTGCCGCCG 892	Db 613 CTCCAAAATCCTCAGTCCTGTGATGACCTTTCCCTACTTATAGGCCTAAGCATGCTGAG 832	CTTCCTTAGCGGCCACATTATATGTTCGCCGTTACGCCTCATCAATATCCGCCATCCCAT

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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.Beq:*

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RESULT 1 US-10-957-135-30 US-Sequence 30, Application US/10957135; GENERAL INFORMATION: APPLICANT: Anderson, David J.	7.5	0.9	23 0.9	23 0.9 400	23 0.9 398	23 0.9 394	23 0.9 385 6	23 0.9 293 6	23 0.9 240	23 0.9 240	0.9 201	23 0.9 152	24 0.9 90100	24 0.9 697	24 0.9 697	24 0.9 574	9 24 0.9 574	24 0.9 368	7 25 1.0 4332	25 1.0 4293	
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (332)...(1297)
US-10-957-135-30
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CURRENT PILING DATE: 2004-09-30

CURRENT FILING DATE: 2004-09-30

PRIOR APPLICATION NUMBER: US 60/222,344

PRIOR FILING DATE: 2000-08-01

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: US 60/202,027

PRIOR APPLICATION NUMBER: US 60/202,027

PRIOR FILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-11-03

PRIOR FILING DATE: 2001-04-19

PRIOR PILING DATE: 2001-04-19

PRIOR PILING DATE: 2001-05-04

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PRIOR PILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: US 10/183,116

PRIOR PILING DATE: 2002-06-26

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NUMBER OF SEQ ID NOS: 109

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APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
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                                                                                                                                                          GCTGTCGGGAAGCAGATTGGAGCAGTGAGGAAGAACCTCTGCCCTGTCAGACAGGACTTT
                                                                                                                                                                                                                                                                                         CGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGC
                                                                                                                                                                                                                                                                                                          CGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGAAGCTGGTTCTCCAGAGGGC 1372
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                                                                                                       GAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCT
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                                                                     GAGAGCAATGCTGCCCTGCCACCCTTGACAATTATATGCATTTTTCTTAGCCTTCTGCCT
                                                                                                                                                                                                                 TCTGCAGGACACGCCTGAGGTGGATGAAGGTGGAGGGTGGCTTCCTCAGGAAACCCCTGGA
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US-10-957-135-15 US-10-957-135-15 ; Sequence 15, Application US/10957135 ; GENERAL INFORMATION:

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APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Dong, Xinzhong
APPLICANT: Simon, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE. 4C1CP1C1
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 99/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 10/489,869
PRIOR APPLICATION NUMBER: US 10/489,869
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEG ID NOS: 109
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 2040
TYDE: NNA
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/202,344
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR PILING DATE: 2001-05-04
PRIOR PILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-957-135-32

; NAME/KEY: CDS
; LOCATION: (328)...(1293)
US-10-957-135-15

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Best Local Similarity
Matches 120; Conserv
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ORGANISM: Homo
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Anderson, APPLICANT: Dong, Xir
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Conservative (
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; Pred. No. 3.9e-42;
0; Mismatches 0;
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; LOCATION: (433)...(1398)
US-10-957-135-32
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; LOCATION: (171)...(1160)
US-10-957-135-17
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TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE 4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR PAILING DATE: 2000-08-01
PRIOR PAPLICATION NUMBER: US 60/202,027
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR PILING DATE: 2001-05-04
                                                                                                         US-10-957-135-62
                                                                                                                              RESULT 5
Sequence 62, Application US/10957135
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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Best Local Similarity
Matches 97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                               976 CTCTTAACAGCAGTGCCAACCCCATCATTTACTTCTTCGTGGGCTC 1021
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Simon, Melvin
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                      DB 6; I
                                                                                                                                                                                                                                                                                  0; Indels
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; ORGANISM: Mus musculus US-10-957-135-62
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US-10-957-135-58
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PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 109
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 58
LENGTH: 2110
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Best Local Similarity
Matches 37; Conserv
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                                                                                  Best Local Similarity Matches 37; Conserv
                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CALTE.4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR FILICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR PRIOR
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PRIOR FILING DATE: 2000-08-01
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CURRENT FILING DATE: 2004-09-30
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TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1C1
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TITLE OF INVENTION: PAIN SIGNALING MOLECULES
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1288 GTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTT 1324
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Simon, Melvin
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                                                                                      Conservative
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; Pred. No. 1e-06;
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                                                                                      Mismatches
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TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-05-04
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PRIOR FILING DATE: 2000-08-01
PRIOR PPLICATION NUMBER: US 60/202,027
PRIOR TILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-17-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-10-04-19
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, David J. APPLICANT: Dong, Xinzhong
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SOFTWARE: FastSEQ for Windows Version 4.0
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                      PRIOR FILING DATE: 2002-0
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2401
TYPE: DNA
ORGANISM: Mus musculus
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nes 37; Conservative 0; Mismatches
                                                               APPLICATION NUMBER: US 09/849,869
FILING DATE: 2001-05-04
APPLICATION NUMBER: US 10/183,116
                                                                                                                               APPLICATION NUMBER: US 09/704,707
FILING DATE: 2000-11-03
APPLICATION NUMBER: US 60/285,493
FILING DATE: 2001-04-19
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APPLICATION NUMBER: US 10/183,116
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      for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Mus musculus
US-10-957-135-54
APPLICANT: Anderson, David J.
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
APPLICANT: Simon, Melvin
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE 4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR APPLICATION NUMBER: US 60/202,027
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US-10-957-135-52
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Best Local Similarity
Matches 34; Conserv
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SOFTWARE: FastSEQ for
SEQ ID NO 72
LENGTH: 2758
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Best Local Similarity
Matches 34; Conserv
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LENGTH: 2093
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PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
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CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
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TITLE OF INVENTION: PAIN SIGNALING MOLECULES
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Simon, Melvin
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100.0%; Pr
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100.0%; Pred. No.
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Pred. No.
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PRIOR FILING DATE: 2000-05-04

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US-10-957-135-24
; Sequence 24, Application US/10957135
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J.
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US-10-957-135-52
                                                                                           RESULT 12
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PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILLING DATE: 2000-08-01
PRIOR PPLICATION NUMBER: US 60/202,027
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR PELICATION NUMBER: US 09/704,707
PRIOR PILLING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR PILLING DATE: 2001-05-04
PRIOR FILLING DATE: 2001-05-04
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GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Dong, Xinzhong
APPLICANT: Zylka, Mark
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SEQ ID NO 52
LENGTH: 1519
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Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
Matches 33; Conserv
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TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
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PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 10/183,116 PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Mus musculus
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                                                                                                                                                                                                      1292 CAACCCCATCATTTACTTCTTCGTGGGCTCCTT 1324
                                                                                                                                                             794 CAACCCCATCATTTACTTCTTCGTGGGCTCCTT 826
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Simon, Melvin
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                                                                                                                                                                                                                                             1.3%; Score 33;
100.0%; Pred. No.
tive 0; Mismatc
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100.0%; Pred. No. 5.2e-05;
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                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                    DB 6; Lt 5.2e-05;
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                                                                                                                                                                                                                                                                                         Length 1738;
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US-10-957-135-1
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                                        SOFTWARE: I
SEQ ID NO 1
LENGTH: 1
                                                                                                                                        CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR FILING DATE: 2000-08-01
PRIOR PELLING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR PILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR APPLICATION NUMBER: US 10/183,116
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PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
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Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Han, Sang-kyou
APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
FILE REFERENCE: CALTE.4C1CP1C1
CURRENT APPLICATION NUMBER: 10/957,135
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 70/772,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, David APPLICANT: Dong, Xinzhong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Mus musculus FEATURE:
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LOCATION: (106)...(1020)
ORGANISM: Mus Musculus
                           TYPE: DNA
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                                                  1088
                                                                                                FastSEQ for Windows Version 4.0
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Simon, Melvin
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100.0%; Prr
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APPLICANT: HYSEQ, INC
ITILE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-042
CURRENT APPLICATION NUMBER: US/10/220,366A
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 27802
SOFTWARE: Custom
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US-10-957-135-64
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                                                                                                                                 APPLICANT: Han, Sang-kyou
TITLE OF INVENTION: PAIN SIGNALING MOLECULES
PILE REFERENCE: CALTE.4C1CP1C1
CURRENT APPLICATION NUMBER: US/10/957,135
CURRENT FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: US 60/222,344
PRIOR TILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: US 60/202,027
PRIOR PRILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 09/704,707
PRIOR PRILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR APPLICATION NUMBER: US 60/285,493
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 2001-04-19
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Best Local Similarity 100.0%; P.
Matches 31; Conservative 0;
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SOFTWARE:
                                         PRIOR APPLICATION NUMBER: US 09/849,869
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 10/183,116
PRIOR FILING DATE: 2002-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Anderson, David J. APPLICANT: Dong, Xinzhong
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LOCATION: (1)...(1010)
OTHER INFORMATION: n = a,t,c or g
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ORGANISM: Homo sapiens
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les 28; Conservative (
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FastSEQ for Windows Version 4.0
                        SEQ ID NOS: 109
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Search completed: October 30, 2004, 03:32:11
Job time : 102 secs
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LENGTH: 1485
                                                                                                                   Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                  TYPE: DNA ORGANISM: Mus musculus
                                                                                           1288 GTGCCAACCCCATCATTTACTTCTTC 1313
                                                             926 GTGCCAACCCCATCATTACTTCTTC 951
                                                                                                                          Conservative
                                                                                                                                      1.0%; Score 26; DB 6;
100.0%; Pred. No. 0.05;
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Perfect score:
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Match
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2618
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gb_gss2:*
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                                      CD24359 AGENCOURT
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CN83776 AGENCOURT
BG210740 RST30287
CN831885 AGENCOURT
CN843633 AGENCOURT
CN843634 AGENCOURT
CN83963 AGENCOURT
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CN83965 AGENCOURT
CN83965 AGENCOURT
BG195197 RST14376
BG195197 RST14376
BG19505 RST15931
AL705589 DKFZp686K
AQ392205 CITB1-E1-
CN843258 AGENCOURT
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AV731610
B74348 CIT-HSP-204
CN835770 AGENCOURT
CN839711 AGENCOURT
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HTM1-025F
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                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
plate: LLAM14285 row: h column: 07
High quality sequence stop: 743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 889)
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                                     /clone="IMAGE:6722551"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
/rell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
/rell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
/rell_line="XR-75-1, MCF7, Site_1: EcoRV; Site_2: Not I;
/rote="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/rote="Vector: pCMY-SPORT6; Site_1: EcoRV; Site_2: Not I;
/rote="Vector: pCMY-SPORT6; Site_1: EcoRV; Site_2: Not I;
/rote="Tector-Image: Note of the content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Manuscript submitted.
                                                                                                                                                                                                              organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                      ocation/Qualifiers
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HL118979
CN192307
CN831931
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AQ587244
CN837998
AQ587244
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CN837998
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AQ888076
T59759
AQ583508
H49498
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p mRNA linear EST 12-NOV-2002 sapiens cDNA clone IMAGE:6722551 5',

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115 2142 B 2142 B 21759 yc13507.r1 AQ583508 RPCI-11 H49498 ym² AG013746 Homo sapi AG013748 Homo sapi BG208126 RST27616 AQ888076 HS 2142 B T59759 yc13507.r1

AG013749 AG013779 AQ696198 AQ587244 CN837998

Homo sapi Homo sapi Homo sapi

AQ192307 CN831931

CN842891 CN839125

HS 2244 A
AGENCOURT
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HS 2142 B
RPCI-11-4
AGENCOURT

CN834097 CN839827 CN843534 AL118979 CN839609

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DKFZp761G AGENCOURT

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                                          Gonzalez,P., Epstein,D.L. and Borras,T. Characterization of gene expression in human trabecular meshwork using single-pass sequencing of 1060 clones Invest. Ophthalmol. Vis. Sci. (2000) In press Contact: Pedro Gonzalez
 Department of Ophthalmology
Duke University
Duke Eye Center, Erwin Rd,
                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 688)
                                                                                                                                                             Homo sapiens
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HTM1-025F1 HTM1 Homo sapiens
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Pred. No. 3.7e-267;
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Catarrhini; Hominidae
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 662)
Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA HTF clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
                                                                                                                                                                                                         AV731610 HTI
AV731610 HTI
AV731610
AV731610.1
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Fax: 919 684 8983
Email: pedro.gonzalez@duke.edu.
Location/Qualifiers
                                                                                                                                                                                              EST.
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                       HTF Homo sapiens
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Pred. No. 5.3e-257;
0; Mismatches 0;
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AUTHORS
TITLE
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Best Local Similarity 99.4%;
Matches 463; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Butheria; Primates; Catarrhini;
1 (bases 1 to 905)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
                                                                                                      Homo sapiens
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clone is available at CHGC in Shanghai.
                                                                                                                  sapiens (human)
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/mol_type="mRNA"
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/lab_host="SOLR"
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o sapiens
                    Gene
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: NDAM447 row: p column: 21
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                                                ACTICCTCTTCCTTAGCGGCCACATTATA 734
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/lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone lib="NHI MGC 180"
/clone lib="NHI MGC 180"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: Not1;
Site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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Pred. No. 1.8e-124;
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 764)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McBilligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K. Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001) BG198766 764 bp mRNA linear EST 21-APR-2 RST18035 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence. BG198766 BG198766.1 GI:13720453 Homo sapiens Homo sapiens (human) Cothren, K., Lo, K.,

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REFERENCE
AUTHORS
TITLE
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Best Local Similarity 100.0%; F
Matches 120; Conservative 0;
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                                                                                                                                                                 CDNA Library Preparation: GPCR Consortium (LLNL) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: IRBI4 row: e column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1009)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT_15864212 NIH_MGC_145 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                               National Cancer Institute / NIH
Bldg. 31 Rm.10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
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216 431 9900
216 361 9596
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Location/Qualifiers
                                                                                                                       quality sequence stop: 464.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression /
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30706611"
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/db_xref="taxon:9606"
/cell_line="HT1080"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 871)

Primaler S. Jackson, P.D., Perry, R.,
                                                                                                                                                                                                                                                                                                                                                                               Contact: Scott J. Cain
Atherays, Inc.
3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
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RST30287 Athersys RAGE Library
BG210740
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High quality sequence stop: 456.
Location/Qualifiers
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milarity 100.0%;
Conservative 0
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/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NoLI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
                 /cione lib="Athersys RAGE Library"
/cione lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/Ibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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/lab_host="DH10B"
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sapiens cDNA,
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Query Match Best Local Similarity

4.4%;

Score 115; DB 4; Length 871; Pred. No. 2.7e-46;

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AUTHORS
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CN831885/c
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Matches 97
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                                                   1347 AACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACA 1383
                                                                                                                          1287 AGTGCCAACCCCATCATTTACTTCCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAG 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 827)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Plate: IRBI4 row: e column: 10
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AGENCOURT 15669850 NIH MGC 145 Homo
IMAGE:30706617 5', mRNA sequence.
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/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:
/note="Vector: pcDNA3.1; Site 1: varies by clone into varies by clone; ORFs were PcR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EccRV-XmmI/XhoI-3', 5'-EccRV-XmmI/NotI-3', EccRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llni.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a.NIH_MGC Library."
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No.
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sapiens cDNA clone
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CN843633/c
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                                                     863 bp 1
AGENCOURT 15864324 NIH MGC 145 Homo
IMAGE:30706618 3', mRNA sequence
CN835944
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High quality sequence stop: 660.
Location/Qualifiers
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Bldg. 31 Rm.10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
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AGENCOURT 15658848 NIH MGC 145 Homo
IMAGE:30706619 5', mRNA sequence.
                 CN835944.1
EST.
                                                   CN835944
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sapiens (human)
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/db_xref="taxon:9606"
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o sapiens
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 835)

NIH-WCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                        AACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACA 1383
                                                                                                                                                                            AGTGCCAACCCCATCATTTACTTCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAG 1346
AACCTGAAGCTGGTTCTCCAGAGGGCTCTGCAGGACA 141
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                                                                                                                                                                                                                                                          Score 97; DB 7; L; Pred. No. 3.8e-37; 0; Mismatches 0;
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                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 895)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                               CN840024 895 bp mRNA linear ES:
AGENCOURT 15864276 NIH MGC 145 Homo sapiens cDNA clone
IMAGE:30706615 3', mRNA sequence.
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Plate: IRBI4 row: e column: 11
High quality sequence stop: 719.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                       Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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CN840024.1 GI:47945679
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Tissue Procurement: GPCR Consortium
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National Cancer Institute / NIH
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/mol type="mxNA"
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/clone="IMAGE:30706618"
/tissue_type="mixed"
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/clone lib="NIH MGC 145"
/clone lib="NIH MGC 145"
/clone lib="NIH MGC 145"
/clone lib="NIH MGC 145"
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmmI/Nbl-3', 5'-EcoRV-XmmI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at tp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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100.0%; Pred. No. 3.8e-37
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 924)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892
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AGENCOURT 15864260 NIH MGC 145 Homo
IMAGE:30706614 3', mRNA sequence.
CN839634
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Email: cgapbs-r@mail:nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
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Plate: IRBI4 row: e column: 08
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/db_xref="taxon:9606"
/clone="TMAGE:307066.5"
/tissue_type="mixed"
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/clone lib="NIH MGC_145"
/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
varies by clone; ORFs were PCR-emplified and cloned into
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmmI/XhoI-3',
5'-EcoRV-XmmI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clones represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
a Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
CDNA Library Preparation: GFCR Consortium
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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1 (Dases 1 to 953)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: IRBI4 row: e column: 09
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Location/Qualifiers
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/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFS were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EccRV-XmmI/XhoI-3', 5'-EccRV-XmmI/NoII-3', EccRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
                                                                 /db_xref="taxon:9606"
/clone="IMAGE:30706616"
                                                                                                                                                                              Location/Qualifiers
                                                                                                             organism="Homo sapiens"
|mol_type="mRNA"
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/tissue_type="mixed"
/lab_host="DH10B"
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/db_xref="taxon:9606"
clone_lib="NIH_MGC_145"
                           lab_host="DH10B"
                                              tissue_type="mixed"
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1294 ACCCCATCATTTACTTCCTTCGTGGGCTCCTTTAGGCAGCGTCAAAATAGGCAGAACCTGA 1353

Query Match
Best Local Similarity
Matches 89; Conserv

3.4%;

Score 89; Pred. No. Mismatches

DB 4; Le 4.2e-33;

Length 184; Indels

Gaps

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 184)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Ways,R., Smith,B., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Aays,R., Smith,B., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Cfenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                         3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 bg
RST14376 Athersys RAGE Library
BG195197
BG195197.1 GI:13716884
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                                                                                                                                                                                                                                                                                                                                                                                                 Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Athersys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11329013
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                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 134.
Location/Qualifiers
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                /mol_type="mRNA"
/db xref="taxon:966"
/cell_line="HT1080"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
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Search completed: October 30, 2004, 00:46:40 Job time : 7932 secs
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1 (bases 1 to 248)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Mhittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115,
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RST15931 Athersys RAGE Library Homo
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                                                                                                 TTTAGGCAGCGTCAAAATAGGCAGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: scain@athersys.com quality sequence stop: 198. Location/Qualifiers
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216 361 9596
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/note="See 'Creation of Genome-wide Protein Expression
/ibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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